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OM protein - protein search, using SW model

Run on: August 20, 2005, 00:10:37 ; Search time 168 Seconds  
(without alignments)  
1258.861 Million cell updates/sec

Title: Perfect score: 2229 US-10-649-852-32

Sequence: 1 MDSTIFELIIDDEFDANCSSL.....SIPTSPTRISPHSIQTAEV 413

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing First 45 summaries

Database : UniProt 03:  
1: uniprot\_sprot:  
2: uniprot\_trembl:  
\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	2229	100.0	413	1	CRF2_XENLA	042603 xenopus lae	
2	2051	92.0	411	2	Q68760	068760 rana catesbe	
3	1963.5	88.1	412	2	Q72722	072722 gallus gall	
4	1904.5	85.4	414	2	Q8AWA1	08AWA1 oncorthynchus	
5	1807	81.1	405	2	Q9BUC1	09BUC1 ameivurus ne	
6	1804	80.9	411	1	CRF2_HUMAN	013324 homo sapien	
7	1796.5	80.6	410	2	Q8WM19	08WM19 tupaia glis	
8	1793	80.4	411	1	CRF2_RAT	047866 rattus norvegicus	
9	1792	80.4	437	2	Q8WM18	08WM18 tupaia glis	
10	1770.5	79.4	431	1	CRF2_MOUSE	060748 mus musculus	
11	1582	71.0	428	1	Q9BUC0	09BUC0 ameivurus ne	
12	1582	71.0	420	1	CRF1_CHICK	090812 gallus gallus	
13	1570.5	70.8	445	2	Q9BUC2	09BUC2 ameivurus ne	
14	1566	70.3	415	1	Q76L18	076L18 macaca mulatta	
15	1564.5	70.2	415	1	CRF1_XENLA	046202 xenopus lae	
16	1564.5	70.2	415	2	Q8K3R2	08K3R2 mesocricetus	
17	1561.5	70.1	434	2	Q7T3S9	07T3S9 fugi rubrip	
18	1559.5	70.0	430	2	Q8AWA2	08AWA2 oncorthynchus	
19	1555.9	69.9	415	2	Q8WM10	08WM10 tupaia glis	
20	1556.5	69.8	415	1	CRF1_MOUSE	035347 mus musculus	
21	1553	69.7	415	2	Q9BGT4	09BGT4 bos taurus	
22	1551.5	69.6	415	1	CRF1_RAT	055353 rattus norvegicus	
23	1541.5	69.2	444	1	CRF1_HUMAN	034998 homo sapiens	
24	1541.5	69.2	447	2	Q8NG71	08NG71 homo sapiens	
25	1539.5	69.1	416	2	Q68Y61	068Y61 rana catesbeiana	
26	1423	68.3	415	1	CRF1_SHEEP	062772 ovis aries	
27	1409.5	63.2	329	2	Q70T6	070T6 cyprinus carpio	
28	950	42.6	277	2	Q8BD9	08BD9 mus musculus	
29	753	33.8	154	2	Q7TS42	097TS42 mesocricetus	
30	721.5	32.4	504	2	Q9V716	09V716 drosophila	
31	716.5	32.1	388	2	Q9V6C7	09V6C7	

## ALIGNMENTS

RESULT 1	CRF2_XENLA	STANDARD:	PRT:	413 AA.
ID	CRF2_XENLA			
AC	Q42603 ;			
DT	15-JUL-1998 (Rel. 36, Created)			
DT	15-JUL-1998 (Rel. 36, Last sequence update)			
DT	25-OCT-2004 (Rel. 45, Last annotation update)			
DE	Corticotropin releasing factor receptor 2 precursor (CRF-R 2) (CRF2)			
DB	(Corticotropin-releasing hormone receptor 2) (CRH-R 2) .			
GN	Xenopus laevis (African clawed frog).			
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;			
OC	Xenopoda; Xenopus.			
OX	NCBI_TaxID=8355;			
RN	SEQUENCE FROM N.A.			
RC	TISSUE=Brain, and Heart; Dietrich K., Palchaudhuri M.R., Spiess J.;			
RX	NAME=CRF2;			
RA	Dautzenberg F.M., Dietrich K., Palchaudhuri M.R., Spiess J.;			
RT	"Identification of two corticotropin-releasing factor receptors from Xenopus laevis with high ligand selectivity: unusual pharmacology of the type 1 receptor.";			
RT	J. Neurochem. 69:1640-1649 (1997).			
RT	"Identification of two corticotropin releasing factor receptors from Xenopus laevis with high ligand selectivity: unusual pharmacology of the type 1 receptor.";			
CC	shows high affinity binding for urotensin I. The activity of this receptor is mediated by G proteins which activate adenylyl cyclase (By similarity).			
CC	-!- SUBCELLULAR LOCATION: Integral membrane protein.			
CC	-!- SIMILARITY: Belongs to the G-protein coupled receptor 2 family.			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a> or send an email to license@isb-sib.ch).			
CC	PRINTS: PRO0249 ; GPCRESERETIN.			
DR	EMBL: Y14037; CRA74364.1. .			
DR	Intertro: IPR000832; GPCR secretin.			
DR	Intertro: IPR001879; hormone receptor.			
DR	PFam: PF00002; 7cm_1.			
DR	PFam: PF02793; HRM_1.			
DR	SMART: SM00018; HormR_1.			
DR	PROSITE: PS00649 ; G-PROTEIN RECEP_F2_1.			
DR	PROSITE: PS00650 ; G-PROTEIN RECEP_F2_2.			
DR	PROSITE: PS00651 ; G-PROTEIN RECEP_F2_3.			
DR	PROSITE: PS050261 ; G-PROTEIN RECEP_F2_4.			
KW	G-protein coupled receptor; Glycoprotein; Signal; Transmembrane.			
FT	SIGNAL 1 ?			
FT	CHAIN 2.			

FT DOMAIN	?	120	Extracellular (Potential).
FT TRANSMEM	121	141	1 (Potential).
FT TRANSMEM	142	150	Cytoplasmic (Potential).
FT TRANSMEM	151	170	2 (Potential).
FT TRANSMEM	171	187	Extracellular (Potential).
FT DOMAIN	188	211	3 (Potential).
FT DOMAIN	212	225	Cytoplasmic (Potential).
FT TRANSMEM	226	247	4 (Potential).
FT DOMAIN	248	266	Extracellular (Potential).
FT TRANSMEM	267	289	5 (Potential).
FT DOMAIN	290	312	Cytoplasmic (Potential).
FT TRANSMEM	313	332	6 (Potential).
FT DOMAIN	333	347	Extracellular (Potential).
FT TRANSMEM	348	367	7 (Potential).
FT DOMAIN	368	413	Cytoplasmic (Potential).
FT CARBOHYD	16	16	N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD	77	77	N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD	89	89	N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD	97	97	N-linked (GlcNAc. . .) (Potential).
SEQUENCE	413 AA;	48458 MW;	DA422FOA96C4626 CRC64;
Query Match Score	100.0%	Score 2229; DB 1;	Length 413;
Best Local Similarity	100.0%	Pred. No. 1e-157;	
Matches 413	0;	Mismatches 0;	
Indels 0;	Gaps 0;		
Qy	1	MDSTIFELIDDEFDANCSDLLDAFQDSFLIHSSESSSPFGFEGPYCSATIDQIGTCMPLSLAG	60
Db	1	MDSTIFELIDDEFDANCSDLLDAFQDSFLIHSSESSSPFGFEGPYCSATIDQIGTCMPLSLAG	60
Qy	61	ELVERCPDSENGIYNTNTVYRECFCENSTWASMNYSOCVPLIDNKRYALHYKIALI	120
Db	61	ELVERCPDSENGIYNTNTVYRECFCENSTWASMNYSOCVPLIDNKRYALHYKIALI	120
Qy	121	INYLGHCSISLALVIAFLICLRSIQLNLTTFILRNIMFLQMDHNTHE	180
Db	121	INYLGHCSISLALVIAFLICLRSIQLNLTTFILRNIMFLQMDHNTHE	180
Qy	181	SNEYVGRCTTIVNYFVVTNFEMMVEGCYLHTA1VMTYSTDKLRKWLFLFIGMCIPSP1	240
Db	181	SNEYVGRCTTIVNYFVVTNFEMMVEGCYLHTA1VMTYSTDKLRKWLFLFIGMCIPSP1	240
Qy	241	IVTWAICLKFLYENEQCWIKEPKYIDYIYQGRVILVLLINFEVLNIVRLMTKLRAST	300
Db	241	IVTWAICLKFLYENEQCWIKEPKYIDYIYQGRVILVLLINFEVLNIVRLMTKLRAST	300
Qy	242	IVTWAICLKFLYENEQCWIKEPKYIDYIYQGRVILVLLINFEVLNIVRLMTKLRAST	300
Db	242	IVTWAICLKFLYENEQCWIKEPKYIDYIYQGRVILVLLINFEVLNIVRLMTKLRAST	300
Qy	301	TSETIQRKAVATLVLPLGLITMFLFTNPGEDDVSQVFIYNSFLQSFGFFVSYF	360
Db	301	TSETIQRKAVATLVLPLGLITMFLFTNPGEDDVSQVFIYNSFLQSFGFFVSYF	360
Qy	361	YCFLNGEVRSAAKRWHRQDHSLRVRVARAMS1PTSPTRISFSIKQTAAV 4 13	
Db	361	YCFLNGEVRSAAKRWHRQDHSLRVRVARAMS1PTSPTRISFSIKQTAAV 4 13	
RESULT 2	Q68760	PRELIMINARY;	PRT; 411 AA.
ID Q68760			
AC Q68760;			
DT 02-OCT-2004 (TREMBrel. 28, Created)			
DT 25-OCT-2004 (TREMBrel. 28, Last sequence update)			
DT 25-OCT-2004 (TREMBrel. 28, Last annotation update)			
DE Corticotropin releasing factor receptor type 2.			
GN Name-CRF-R2;			
OS Gallus gallus (Chicken).			
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;			
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;			
OC Gallus.			
NCBI_TaxID=9031;			
RN [1]			
RP SEQUENCE FROM N.A.			
RC TISSUE=Cerebellum.			
RX PubMed=12970166, DOI=10.1210/en.2003-0526;			
RA Ito Y., Ogata D., Hasunuma I., Kitoryama S.;			
RT "molecular cloning of two corticotropin releasing factor receptors from bullfrog";			
RT Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.			

RL	Endocrinology 144:5537-5544 (2003).	DR	InterPro; IPR003053; CRF2 receptor.
DR	EMBL; AJ057031; CAD8534_2;	DR	InterPro; IPR003051; CRF receptor.
DR	GO; GO:001020; C:membrane; IEA.	DR	InterPro; IPR00832; GPR secretin.
DR	GO; GO:0004930; F:G-protein coupled receptor activity; IEA.	DR	InterPro; IPR001879; hormone receptor.
DR	GO; GO:0004872; F: receptor activity; IEA.	DR	Pfam; PF00002; 7tm_2; 1.
DR	InterPro; IPR000832; GPCR secretin.	DR	Pfam; PF02793; HRM_1.
DR	InterPro; IPR001879; hormone receptor.	DR	PRINTS; PR01281; CRFRECEPTOR.
DR	PFam; PF00022; 7tm_2; 1.	DR	PRINTS; PR00239; GPCRSECRETIN.
DR	PRINTS; PR02793; HRM_1.	DR	SMART; SM00008; HormR_1.
DR	SMART; SM00249; GPCRESECRETIN.	DR	PROSITE; PS00650; G PROTEIN RECEP_F2_2; 1.
DR	SMART; SM00008; HormR_1.	DR	PROSITE; PS50227; G PROTEIN RECEP_F2_3; 1.
DR	PROSITE; PS000650; G PROTEIN RECEP_F2_2; 1.	DR	PROSITE; PS50261; G PROTEIN RECEP_F2_4; 1.
DR	PROSITE; PS50227; G PROTEIN RECEP_F2_3; 1.	KW	Receptor.
DR	PROSITE; PS50261; G PROTEIN RECEP_F2_4; 1.	KW	SEQUENCE 414 AA; 48339 MW; 11FB2E9B4481CCC2 CRC64;
SQ	SEQUENCE 412 AA; 48095 MW; 641B269460EC4041 CRC64;	Query Match	85.4%; Score 1904.5; DB 2; Length 414;
	Query Match 88.1%; Score 1963.5; DB 2; Length 412;	Best Local Similarity	83.8%; Pred. No. 1.4e-133;
	Best Local Similarity 87.7%; Pred. No. 5.7e-138;	Matches 347; Conservative 30; Mismatches 36; Indels 1; Gaps 1;	Matches 347; Conservative 30; Mismatches 36; Indels 1; Gaps 1;
	Matches 362; Conservative 22; Mismatches 28; Indels 1; Gaps 1;	Qy	1 MDSTIFELIDEFDANCSLLAFQDSPIHSSSSRFQEGPYCSATIDQIGTCWRSLAG 60
Qy	1 MDSTIFELIDEFDANCSLLAFQDSPIHSSSSRFQEGPYCSATIDQIGTCWRSLAG 60	Db	1 MDATIYQIIIFEGFPNCNSYMDSFQDSFYENASPSLMDFFGLYCNATTDEGTCPKNSNT 60
Db	1 MDVTISQFLIEFEDANSSLL-QETVTELESFISIFQFGLYCNATIDQIGTCWPRASAG 59	Qy	60 GELVERPCPDSSFGNRYNTTRNVTYRECFTGWAHMMNTSQCVPLDNLKRYKIAL 119
Qy	61 ELVERPCPDSSFGNRYNTTRNVTYRECFTGWAHMMNTSQCVPLDNLKRYKIAL 120	Db	61 GRMVEBPCPETINGKNTFSAYBECIDNGTWAHMMNTSQCVPLDNLKRYKIAL 120
Db	60 KLVVERPCPEFFGIGKNTNTNAYRECGLNGTWSKNSSQCEPILDKKRYAHYKIAL 119	Qy	120 INYLGHCISLALIAVIAPIFLFLCIRSICRLRNTHWNLTTFLRNIMWFLQMDIENIHE 180
Qy	121 INYLGHCISLALIAVIAPIFLFLCIRSICRLRNTHWNLTTFLRNIMWFLQMDIENIHE 180	Db	121 INYLGHCISVGALIAVAFILFLCIRSICRLRNTHWNLTTFLRNIMWFLQMDIENIHE 180
Db	120 INYLGHCISVGALIAVAFILFLCIRSICRLRNTHWNLTTFLRNIMWFLQMDIENIHE 179	Qy	180 ESNEWYCRITITIINYFVFTVNFPMFVEGCVLHTAVMVTSTDKRKWVFLFIGCIPSP 239
Qy	181 SNEWVCRITITIINYFVFTVNFPMFVEGCVLHTAVMVTSTDKRKWVFLFIGCIPSP 240	Db	181 ESNEPMCRITITIINYFVFTVNFPMFVEGCVLHTAVMVTSTDKRKWVFLFIGCIPCP 240
Db	180 SNEWVCRITITIINYFVFTVNFPMFVEGCVLHTAVMVTSTDKRKWVFLGWC1PCP1 239	Qy	240 IIVTWAICKLKYENEOCWIKEPGEKIDYQGRVYLVLLINFVFLNIVRLMTKLRS 299
Qy	241 IIVTWAICKLKYENEOCWIKEPGEKIDYQGRVYLVLLINFVFLNIVRLMTKLRS 300	Db	241 IIVTWAICKLKYENEOCWIKEPGEKIDYQGRVYLVLLINFVFLNIVRLMTKLRS 300
Db	240 IIVTWAICKLKYENEOCWIKEPGEKIDYQGRVYLVLLINFVFLNIVRLMTKLRS 299	Qy	300 TTSETIYQKAVKATVLPLGLITMFLFVNPGEDDYVSQIVYIYFNSFLQSFQGFFFVSV 360
Qy	301 TTSETIYQKAVKATVLPLGLITMFLFVNPGEDDYVSQIVYIYFNSFLQSFQGFFFVSV 360	Db	301 TTSETIYQKAVKATVLPLGLITMFLFVNPGEDDYVSQIVYIYFNSFLQSFQGFFFVSV 360
Db	300 TTSETIYQKAVKATVLPLGLITMFLFVNPGEDDI.SQIVYIYFNSFLQSFQGFFFVSV 359	Qy	360 FYCFINGEVSAARIKWRDHSILVRVARAMSILPTSPTRISHSIKQTAAY 413
Qy	361 YCFINGEVSAARIKWRDHSILVRVARAMSILPTSPTRISHSIKQTAAY 412	Db	361 FYCFINGEVSAARIKWRDHSILVRVARAMSILPTSPTRISHSIKQTAAY 414
RESULT 5			
Q98UC1	PRELIMINARY; PRT; 414 AA.	ID	Q98UC1 PRELIMINARY; PRT; 405 AA.
AC		AC	Q98UC1; PRELIMINARY; PRT; 405 AA.
DT	01-MAR-2003 (TREMBLrel. 23, Created)	DT	01-JUN-2001 (TREMBLrel. 17, Created)
DT	01-MAR-2003 (TREMBLrel. 23, Last sequence update)	DT	01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT	01-OCT-2003 (TREMBLrel. 25, Last annotation update)	DT	01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE	Corticotropin-releasing factor receptor type 2.	DE	Corticotropin releasing factor receptor 2.
GS	Name=crfr2;	OS	Ameiurus nebulosus.
OC	Oncorhynchus keta (Chum salmon).	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Buteleostei; Siluriformes; Ictaluridae; Ameiurus.
OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Buteleostei; Siluriformes; Ictaluridae; Ameiurus.	OX	NCBI_TaxID=27778;
RN	NCBI_TaxID=8018;	RN	SEQUENCE FROM N.A.
RP	SEQUENCE FROM N.A.	RP	SEQUENCE FROM N.A.
RR	TISSUE=Heart;	RR	SEQUENCE FROM N.A.
RC	Submitted (MAY 2000) to the EMBL/GenBank/DBJ databases.	RC	SEQUENCE FROM N.A.
RI	Submitted (MAY 2000) to the EMBL/GenBank/DBJ databases.	RI	SEQUENCE FROM N.A.
DR	EMBL; AJ277158; CAC8154.1;	DR	SEQUENCE FROM N.A.
DR	GO; GO:00016020; C:membrane; IEA.	DR	SEQUENCE FROM N.A.
DR	GO; GO:0004910; F:G-protein coupled receptor activity; IEA.	DR	SEQUENCE FROM N.A.
DR	GO; GO:0004872; F: receptor activity; IEA.	DR	SEQUENCE FROM N.A.

DR	GO:0004872; F: receptor activity; IEA.
DR	InterPro: IPR010053; CRF2 receptor.
DR	InterPro: IPR003051; CRF receptor.
DR	InterPro: IPR008322; GPCR receptor.
DR	InterPro: IPR01879; hormone receptor.
DR	Pfam: PF00002; 7tm_2; 1.
DR	Pfam: PF02793; HRM_1.
DR	PRINTS: PRO1279; CRFRECEPTOR.
DR	PRINTS: PRO1281; CRFRECEPTOR2.
DR	PRINTS: PRO0249; GPCRESECRETIN.
DR	SMART: SM00008; HormR_1.
DR	PROSITE: PS00650; G-PROTEIN RECEP_P2_2; 1.
DR	PROSITE: PS00227; G-PROTEIN RECEP_P2_3; 1.
DR	PROSITE: PS00261; G-PROTEIN RECEP_P2_4; 1.
KW	Receptor.
SQ	405 AA; 46823 MW; E05896BCPEAD5CC5 CRC64;
Query Match	81.1%; Score 1807; DB 2; Length 405;
Best Local Similarity	79.9%; Pred. No. 2.4e-126;
Matches	33; Mismatches 33; Indels 8; Gaps 2;
Qy	1 MDSTTFLIDEFDDANSCLLDAFDQDSLHSSSESSPFPFGSPYCSATIDQIQTGTCWPRSLAG 60
Db	1 MEVSLIENE-SVVEKSLSLAEGDAGDAYGNSDAL----YCNATDAEIGTGPFRSGAG 52
Qy	61 ELYVERCPDSEFNIGIRYNTTRAVYRECENGFTWASVNNYSOCVPTLDKRYALHYKIAI 120
Db	53 RYVAPRCDFGKVNSKTRSAVRECLENGWAPKINYSSCPELEKSKYVPHKIAI 112
Qy	121 INVIGHCISLALVIAFLCLPSIPLCLNLTQHNLITFLINMMLWQDMDHNTHE 180
Db	113 INYLGHCISVGALVIAFVFLCLRSICLRNLVHNLITFLINMMLWQDMDHNTHE 172
Qy	181 SNEVWVRCRITIYNYFVVTNFVWMTFVEGCVLHTATWVTSKDKRKVWPLFICGICPSI 240
Db	173 RHEPWCLLITTYVNNYFVVTNFVWMTFVEGCVLHTATWVTSKDKRKVWPLFICGICPSI 232
Qy	241 IYTWAICKLFLYENEOQWIGKEFGKYLDIYTIVGRTVILLINFEVLFLNIVRLMTKLRAST 300
Db	233 IIAWAGKLYNENEHQCMFGKEPGKTYDIIYTIVGPVIVLILNFEVLFLNIVRLMTKLRAST 292
Qy	301 TSETTIVQYRKAVATLWLIPIJGLTVMUFFYNGEDEIQSIVFELNSFLOSFOGFYVSF 360
Db	293 TSETTIVQYRKAVATLWLIPIJGLTVMUFFYNGDDDISQIVFIVNSFLQSFGQFFVSFV 352
Qy	361 YCPLNGEVRSAAKRKWFRWQDHSLVYVARAMSTSPTSPRISPSIKQTAAV 413
Db	353 YCPLNGEVRSAAKRKWFRWQDHSLVYVARAMSTSPTSPRISPSIKHETTAV 405
RESULT 6	
CRF2_HUMAN	
ID	CRF2_HUMAN
STANDARD	
PRT	411 AA.
AC	Q133274; Q43461; Q99411.
Q1-NOV-1997 (Rel. 35, Created)	
DT	30-MAY-2000 (Rel. 39, Last annotation update)
DT	25-OCT-2004 (Rel. 45, Last annotation update)
DE	Corticotropin-releasing factor receptor 2 precursor (CRF-R 2) (CRF2)
DE	(Corticotropin-releasing hormone receptor 2) (CRH-R 2).
GN	Name=CRF2R2; Synonyms=CRF2R, CRH2R;
OS	Homo sapiens (Human).
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TAXID	=9606;
RN	[1]
RP	SEQUENCE FROM N.A. (ISOFORM CRF2-ALPHA).
RX	Medline=96107120; PubMed=853664; DOI=10.1210/en.137.1.72;
RA	Lia C.W., Lovenberg T.W., Barry G., Oltersdorff T., Grigoriadis D.E.,
RA	de Souza E.B.;
RT	"Cloning and characterization of the human corticotropin-releasing factor-2 receptor complementary deoxyribonucleic acid."
RT	Endocrinology 137:72-77 (1996).
RL	[2]

PRINTS; PRO0249; GPCRSECRETIN.

SMART; SM00008; HormR; 1.

PROSITE; PS00649; G-PROTEIN RECP F2; 1.

PROSITE; PS00650; G-PROTEIN RECP F2; 1.

PROSITE; PS0227; G-PROTEIN RECP F2; 1.

PROSITE; PS00261; G-PROTEIN RECP F2; 1.

Alternative splicing; G-protein coupled receptor; Glycoprotein;

KW Signal; Transmembrane.

FT SIGNAL 1 17 Potential.

FT CHAIN 18 411 Corticotropin releasing factor receptor

FT 2. Extracellular (Potential).

FT DOMAIN 18 118 Extracellular (Potential).

FT TRANSMEM 119 139 1 (Potential).

FT DOMAIN 140 148 Cytoplasmic (Potential).

FT TRANSMEM 149 168 2 (Potential).

FT DOMAIN 169 185 Extracellular (Potential).

FT TRANSMEM 186 3 (Potential).

FT DOMAIN 210 223 Cytoplasmic (Potential).

FT TRANSMEM 224 245 4 (Potential).

FT DOMAIN 246 264 Extracellular (Potential).

FT TRANSMEM 265 287 5 (Potential).

FT DOMAIN 288 310 Cytoplasmic (Potential).

FT TRANSMEM 311 330 6 (Potential).

FT DOMAIN 331 345 Extracellular (Potential).

FT TRANSMEM 346 365 7 (Potential).

FT CARBOHYD 366 411 N-Linked (GlcNAc . . .) (Potential).

FT CARBOHYD 74 74 N-Linked (GlcNAc . . .) (Potential).

FT CARBOHYD 86 86 N-Linked (GlcNAc . . .) (Potential).

FT CARBOHYD 94 94 N-Linked (GlcNAc . . .) (Potential).

FT VARSPLIC 1 34 MDALLISLLEANCSTALAAELLDDMGCPDPE -> MRG PSEPPGLLIVPHMLLCLLCLLPLQTAQGOSQMPKDPLW ALLEQYCHTMLTTLNLS in isoform CRF2-beta).

FT /PTId=VSP 001999.

FT MDALLISLLEANCSTALAAELLDDMGCPDPE -> MGR EPMDRDLGFPQLFCQ (in isoform CRF2-

FT gamma).

FT CONFLICT 185 185 R -> H (in Ref. 1).

FT SEQUENCE 411 AA; 47687 MW; 96B99939594CF0F CRC64;

Query Match 80.9%; Score 1804; DB 1; Length 411;

Best Local Similarity 80.0%; Pred. No. 4.1e-126;

Matches 333; Conservative 33; Mismatches 42; Indels 8; Gaps 4;

Qy 1 MDSTIFFIIDEFDANSLLDAQDFSHSESSSEFFGEGP - YCSATIDQIGTCMPSRL 58

Db 1 MDALLHSLL--EANCSL--ALAEELLDDMGCPDPEGPySCTNLDQIGTCMPSRL 55

Qy 59 AGELVERPCDPSFGIRNTTRNVTRECPENGWASHWNNYSCQVPLDNN-KRYALHYKI 117

Db 56 AGALVERPPEYFGVKTNTTRNVTRECLENGWASHWNNYSCQVPLDNN-KRYALHYKI 117

Qy 118 ALINYLGHICSTIALVIAFLFLCLRSRCLNTIHNWLTTFLRNIMWFLQDHE 177

Db 116 ALVNVNLGHCVSVAFLFLALRSRCLRNVHNWLTTFLRNIMWFLQDHE 175

Qy 238 SPLITVWAIKLFYENQCGWIGKEPKI1DYLQGRVILVLLINFVFLNIRLMTKL 297

Db 236 FPIIAWAIKLYTENQCGWFGKEPGDLYDYLQGPILVLLINFVFLNIRLMTKL 295

Qy 178 IHESENEWCRCITIYNNFVNTNPFMVEGCVLHTAUMTYSTDKLKRKWLFLFIGCIP 237

Db 176 VHESENEWCRCITIYNNFVNTNPFMVEGCVLHTAUMTYSTERLKCLFLFIGCIP 235

Qy 298 ASTSETIQRKAVKATLVLPLPLGITYMFLFFYNGEEDDSQIVFIFNSFLOSFOGFFV 357

Db 296 ASTSETIQRKAVKATLVLPLPLGITYMFLFFNPGEDDSQIVFIFNSFLOSFOGFFV 355

Qy 358 SVFVCFPLGEVRSARKWHRWQDHHSURVARAMSPTSPTRISFSIKQTAAV 413

Db 356 SVFVCFPLGEVRSARKWHRWQDHHSURVARAMSPTSPTRISFSIKQTAAV 411

PRINTS; PRO1281; CRPRECEPTOR2.

PRINTS; PRO0049; GPCRSECRETIN.

SMART; SM00008; HormR; 1.

PROSITE; PS00649; G-PROTEIN RECEP F2; 1.

PROSITE; PS00650; G-PROTEIN RECEP F2; 2.

PROSITE; PS05026; G-PROTEIN RECEP F2; 3.

PROSITE; PS50261; G-PROTEIN RECEP F2; 4.

PRINTS; PRO1279; CRPRECEPTOR.

PRINTS; PRO0049; GPCRSECRETIN.

Sequence 410 AA; 47613 MW; 09AB66031A63DDC CRC64;

Query Match 80.6%; Score 1796.5; DB 2; Length 410;

Best Local Similarity 79.0%; Pred. No. 1.5e-125;

Matches 328; Conservative 34; Mismatches 46; Indels 7; Gaps 3;

Qy 1 MDSTIFFIIDEFDANSLLDAQDFSHSESSSEFFGEGP - YCSATIDQIGTCMPSRL 58

Db 1 MDALLHSLL--EANCSL--ALAEELLDDMGCPDPEGPySCTNLDQIGTCMPSRL 55

Qy 59 AGELVERPPEYFGVKTNTTRNVTRECLENGWASHWNNYSCQVPLDNN-KRYALHYKI 118

Db 56 AGALVERPPEYFGVKTNTTRNVTRECLENGWASHWNNYSCQVPLDNN-KRYALHYKI 115

Qy 119 LIINYLGHICSTIALVIAFLFLCLRSRCLNTIHNWLTTFLRNIMWFLQDHE 178

Db 116 LVNVNLGHCVSVAFLFLALRSRCLRNVHNWLTTFLRNIMWFLQDHE 175

Qy 179 HESNEWCRCITIYNNFVNTNPFMVEGCVLHTAUMTYSTDKLKRKWLFLFIGCIP 238

Db 176 HESNEWCRCITIYNNFVNTNPFMVEGCVLHTAUMTYSTERLKCLFLFIGCIP 235

Qy 239 SPLITVWAIKLFYENQCGWIGKEPKI1DYLQGRVILVLLINFVFLNIRLMTKL 298

Db 236 PIIAWAIKLYTENQCGWFGKEPGDLYDYLQGPILVLLINFVFLNIRLMTKL 295

Qy 299 STSETIQRKAVKATLVLPLPLGITYMFLFFYNGEEDDSQIVFIFNSFLOSFOGFFV 358

Db 296 STSETIQRKAVKATLVLPLPLGITYMFLFFNPGEDDSQIVFIFNSFLOSFOGFFV 355

Qy 359 VEVCFPLGEVRSARKWHRWQDHHSURVARAMSPTSPTRISFSIKQTAAV 413

356 VEVCFENGEVRSAIRKRMWHRMODHHSTI.RVPUVARAMSIPTSPTRISEHSHIKOTAAV 410

Corticotropin releasing factor receptor 2									
PT	CHAIN	18	411	Corticotropin releasing factor receptor 2					
PT	DOMAIN	18	118	Extracellular	Potential				
PT	TRANSMEM	119	139	1	(Potential)				
PT	DOMAIN	140	148	Cytoplasmic	(Potential)				
PT	TRANSMEM	149	168	Extracellular	(Potential)				
PT	DOMAIN	169	185	2	(Potential)				
PT	TRANSMEM	186	209	3	(Potential)				
PT	DOMAIN	210	223	Cytoplasmic	(Potential)				
PT	TRANSMEM	224	245	4	(Potential)				
PT	DOMAIN	246	264	Extracellular	(Potential)				
PT	TRANSMEM	265	287	5	(Potential)				
PT	DOMAIN	288	310	Cytoplasmic	(Potential)				
PT	TRANSMEM	311	330	6	(Potential)				
PT	DOMAIN	331	345	Extracellular	(Potential)				
PT	TRANSMEM	346	365	7	(Potential)				
PT	DOMAIN	366	411	Cytoplasmic	(Potential)				
PT	CARBOHYD	41	41	N-Linked	(GICNAC . . .)	(Potential)			
PT	CARBOHYD	74	74	N-Linked	(GICNAC . . .)	(Potential)			
PT	CARBOHYD	86	86	N-Linked	(GICNAC . . .)	(Potential)			
PT	CARBOHYD	94	94	N-Linked	(GICNAC . . .)	(Potential)			
PT	VARSPLIC	1	34	MDALLLUSLEANCSSLABELLLDGGEPDPLWTILEL PESLPSLQILCLYLISLPLQVQAPGRPLQDPLWTILEL CHRTPTNNS (in isoform CRF2-beta)					
PT				/PTID=vSP_002001					
PT	SEQUENCE	411	AA;	47706	MW;	1C6B85801BC94469	CRC64;		
SEQUENCE FROM N.A.									
PT	SEQUENCE	Sprague-Dawley; TISSUE=Hypothalamus, and Lung;		Score 1793;	DB 1;	Length 411;			
PT	STRAIN	NAME=Crhr2; Synonyms=Crt2r;		Best Local Similarity	80.0%;	Pre. No. 2,7e-125;			
PT	MEDLINE	Rattus norvegicus (Rat);		Matches 333;	Conservative	Mismatches 45;	Indels 8;	Gaps 8;	
PT	LOVENBERG	T.W., Liaw C.W., Grigoriadis D.E., Clevenger W., Chalmers D.T., de Souza E.B., Oltersdorf T.,							
PT	PROC	Natl. Acad. Sci. U.S.A. 92:5759-5759 (1995).							
PT	LOVENBERG	T.W., Liaw C.W., Grigoriadis D.E., Clevenger W., Chalmers D.T., de Souza E.B., Oltersdorf T.,		QY	1	MDSTTIPETIDDEFANCSLDAQDFSPFLHSESSSEFFGEGP--YCSATLDOIGTCWPRS			
PT	PROC	Natl. Acad. Sci. U.S.A. 92:836-840 (1995).		DB	1	MDA--LILSLBANCNSL--ALAEELLDGGEPPDDEGPYSYCNTLTDQIGTCWQS			
PT	ERRATUM.			QY	59	AGLIVERCPDSDPGIRNNTANVRECPENGWASATYKSSACVPLDNK-RKVALHYK			
PT	ERRATUM.			DB	56	PGALIVERCPEPENGIKYNTTNAVRECLENGWASRINYSHCEPLIDDKQRYKDLYR			
PT	ERRATUM.			QY	118	ALINYLGHCISIILALVIAFLFLCLRSICRNIIWNLTFLRNIMWFLQMIDH			
PT	ERRATUM.			DB	116	ALINYLGCVSVALVAFPLFLVRSICRNIVANLITFLRNITFLRNITFLQDIDH			
PT	ERRATUM.			QY	178	IHSNEWCRCTTINYFVFTNFVMEVEGCYLHTAIVMTYSTDQLRKWVFLFIGC1			
PT	ERRATUM.			DB	176	VHSNEWCRCTVFLFVFTNFVMEVEGCYLHTAIVMTYSTEHLRKWVFLFIGC1			
PT	ERRATUM.			QY	238	SPLIVTMACKLYENEQWIGKEPGKIDYIYQGRVILVLLNFVFLNIVFLNIVFLMVKL			
PT	ERRATUM.			DB	236	CPLIVAWVGKLYENEQWFGKEPGLDLYIYQGPFLVLLNFVFLNIVFLMVKL			
PT	ERRATUM.			QY	298	ASTTSETIQYRKAVATLVLPLGITYMFLFVNPGEDDSQVYFVFNFSFQGFF			
PT	ERRATUM.			DB	296	ASTTSETIQYRKAVATLVLPLGITYMFLFVNPGEDDSQVYFVFNFSFQGFF			
PT	ERRATUM.			QY	358	SVYFCFLNGEVRSAAKRKWHRMODHHSLRVYARAMSTPTSPTRSPHSIKQTAAV 41			
PT	ERRATUM.			DB	356	SVYFCFFNGEVRSALRKWHRMODHHLRVPARAMSPTSPTRSPHSIKQTAAV 41			
PT	RESULT	9							
PT	QBWML8	PRELIMINARY;							
PT	QBWML8	AC							
PT	QBWML8	DT	01-MAR-2002	(TREMBLrel. 20, Created)					
PT	QBWML8	DT	01-MAR-2002	(TREMBLrel. 20, Last sequence update)					
PT	QBWML8	DT	01-MAR-2004	(TREMBLrel. 26, Last annotation update)					
PT	QBWML8	DE		Corticoropin releasing factor type 2B receptor.					
PT	QBWML8	GN		Name=crl2;					
PT	QBWML8	OS		Tupaia gila belangeri (Common tree shrew).					
PT	QBWML8	OC		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
PT	QBWML8	OC		Mammalia; Eutheria; Scandentia; Tupaiae; Tupaidae; Tupaia; Tupaia.					
PT	QBWML8	OX		NCBI TaxID:37347;					
PT	QBWML8	OX		Signal; Transmembrane					
PT	QBWML8	OX		Potential					

[1]	SEQUENCE FROM N.A.	Mus musculus (Mouse)
	Medline=9288234; PubMed=10336722;	OC
	Patra M.R.; Hauger R.L.; Wille S.; Fuchs E.; Dautzenberg F.M.;	OC
	"Isolation and pharmacological characterization of two functional	OC
	splice variants of corticotropin-releasing factor type 2 receptor from	OC
	the tree shrew ( <i>Tupaia belangeri</i> )."	OC
[2]	SEQUENCE FROM N.A.	NCBI_TaxID=10090; [1]
	Dautzenberg F.M.; Submitted (DEC 2001) to the EMBL/GenBank/DDBJ databases.	SEQUENCE FROM N.A.
	EMBL; A412243; CAD19579; -.	RC TISSUE:Heart;
	GO: GO:0016020; C:membrane; IEA.	RX MEDLINE=95224061; PubMed=7708757;
	GO; GO:004930; F:G-protein coupled receptor activity; IEA.	RA Perrin M.; Donaldson C.; Chen R.; Blount A.; Berggren T.,
	GO; GO:004872; F:receptor activity; IEA.	RA Bilezikjian L.; Swithenbo P.; Vale W.;
	PRINTS; PR00002; 7tm; 2; 1.	RT "Identification of a second corticotropin-releasing factor receptor
	PRINTS; PR01281; CFRECREPT02.	RT gene and characterization of a cDNA expressed in heart.";
	PRINTS; PR00249; GRCSECRETIN.	RL Proc. Natl. Acad. Sci. U.S.A. 92:2969-2973(1995).
	SEQUENCE 437 AA; 50329 MW; E4721B7D880E1B07 CRC64;	RN RP SEQUENCE FROM N.A.
	Query Match Score 80.4%; Best Local Similarity 85.1%; Pred. No. 3.4e-125; Matches 320; Conservative 29; Mismatches 25; Indels 2; Gaps 1;	RC STRAIN:BALB/C; TISSUE:Heart;
	40 GP-YCSATIDQIGTCMPSRLAGELYVERCPDIFSGNTRVYRECENGFTWASMN 97	RX MEDLINE=96015396; PubMed=7565810; DOI=10.1210/me.9.5.637;
	62 GPYSTNTTLDQIGTCMPSRLAGALLERCPBYFNGKINTRVYRECENGFTWASRN 121	RA Stenzel P.; Kesterson R.; Yeung W.; Cone R.D.; Rittenberg M.B.,
	98 YSQCYPILDKRYKALHYKIALINYLGHCTISILAVIAFLFLCLRSIRCNTHWNL 157	RA Stenzel-Poore M.P.;
	122 YSQCYPILDKRYKALHYKALYHMAAFLVAVFLGCVSMAALVAVFLGCVSMAALV 181	RT "Identification of a novel murine receptor for corticotropin-releasing
	158 ITTFILRNWFLQLQIDHNEISNEWCRGTTTINYKFTTNPFFMVEGCCYLTIAVM 217	RT hormone expressed in the heart.";
	182 ITTFILRNWFLQLQIDHTEHESNEWCRGTTTINYFVYTTFNFMVEGCCYLTIAVM 241	RL Mol. Endocrinol. 9:637-645(1995).
	218 TYSTDFKLKRYFLGICNCPSPILTWAIKFLKLYENQWQKIGKEPGRKIDTYQGKVLV 277	CC -1- FUNCTION: This is a receptor for corticotropin releasing factor.
	242 TYSTDFKLKRYFLGICNCPSPILTWAIKFLKLYENQWQKIGKEPGLDLYYQGPILW 301	CC -1- Shows high-affinity CRF binding. Also binds to urocortin 1, II and
	278 LLINNFYFLENIVRLMTKLRASTTSETIQKRAVKATLVLPLIGITMYLFFVNPGGRDDV 337	CC -1- The activity of this receptor is mediated by G proteins which
	302 LLINNFYFLENIVRLMTKLRASTTSETIQKRAVKATLVLPLIGITMYLFFVNPGDDL 361	CC -1- activate adenylyl cyclase.
	338 SQIVFVFNPSFLQSFQFFVSYCFINGEVRSAAKRWKQDHSLRVYARAMSIP 397	CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
	362 SQIVFVFNPSFLQSFQFFVSYCFINGEVRSAAKRWKQDHSLRVYARAMSIP 421	CC -1- TISSUE SPECIFICITY: Highly expressed in the heart. Also expressed
	398 SPTRISFHSIKOTAAV 413	CC in lungs, skeletal muscle, gastrointestinal tract, epididymis, and
	422 SPTRISFHSIKOTAAV 437	CC brain.
		CC -1- SIMILARITY: Belongs to the G-protein coupled receptor 2 family.
		CC This SWISS-PROT entry is copyright. It is produced through a collaboration
		CC between the Swiss Institute of Bioinformatics and the EMBL outstation
		CC the European Bioinformatics Institute. There are no restrictions on its
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		CC
		CC EMBL; U17858; AAA68026_1; -
		CC DR EMBL; U21729; AAC52174_1; -
		CC DR EMBL; U19939; AAC52243_1; -
		CC PIR; A56726; A56726.
		CC DR PIR; I49149; I49149.
		CC DR PIR; I49229; I49229.
		CC DR MGI; 894312; Crhr2.
		CC DR GO; GO:0015056; F:corticotropin-releasing factor receptor ac. . . ; IDA.
		CC DR InterPro; IPR000832; GPCR_Secretin.
		CC DR InterPro; IPR001819; hormn_receptor.
		CC DR Pfam; PF00002; 7tm_2_1.
		CC DR Pfam; PF02793; HRN_1.
		CC DR PRINTS; PR00249; GPCRSRERETIN.
		CC DR SMART; SM00088; HormR_1.
		CC DR PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; 1.
		CC DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; 1.
		CC DR PROSITE; PS50227; G_PROTEIN_RECEP_F2_3; 1.
		CC DR PROSITE; PS50228; G_PROTEIN_RECEP_F2_4; 1.
		CC KW G:protein coupled receptor; Glycoprotein; Signal; Transmembrane.
		CC FT SIGNAL_1 24 Potential.
		CC FT CHAIN 25 431 Corticotropin releasing factor receptor
		CC FT DOMAIN 25 138 Extracellular (Potential).
		CC FT TRANSMEM 139 159 Synonyms=Crf2r1
		CC FT TRANSMEM 139 159 R2).

FT	DOMAIN	160	168	Cytoplasmic (Potential).	RX	RA	MEDLINE-21066341; PubMed=11145609; DOI=10.1210/en.142.1.446;
FT	TRANSEM	169	188	2 (Potential).		Araci M., Assil I. O., Abou-Samra A. B.	
FT	DOMAIN	189	205	Extracellular (Potential).		"Characterization of three corticotropin-releasing factor receptors in	
FT	TRANSEM	206	229	3 (Potential).		catfish: a novel third receptor is predominantly expressed in	
FT	TRANSEM	230	243	Cytoplasmic (Potential).		pituitary and urophysis."	
FT	TRANSEM	244	265	4 (Potential).		Endocrinology 142:446-454 (2001).	
FT	DOMAIN	266	284	Extracellular (Potential).		DR	
FT	TRANSEM	285	307	5 (Potential).		DR	
FT	DOMAIN	308	330	Cytoplasmic (Potential).		GO	
FT	TRANSEM	331	350	6 (Potential).		GO	
FT	TRANSEM	351	365	Extracellular (Potential).		GO	
FT	TRANSEM	366	385	7 (Potential).		InterPro	
FT	DOMAIN	386	431	Cytoplasmic (Potential).		IPR003051; CRF receptor.	
FT	CARBOHD	52	52	N-linked (GlcNAc. . .) (Potential).		IPR00832; GPCR receptor.	
FT	CARBOHD	61	61	N-linked (GlcNAc. . .) (Potential).		InterPro	
FT	CARBOHD	94	94	N-linked (GlcNAc. . .) (Potential).		IPR0016020; C:membrane; IEA.	
FT	CARBOHD	106	106	N-linked (GlcNAc. . .) (Potential).		IPR004872; F:receptor activity; IEA.	
FT	CARBOHD	114	114	N-linked (GlcNAc. . .) (Potential).		IPR0016020; F:receptor activity; IEA.	
FT	CONFLICT	3	5	TPG -> QOI (in Ref. 2).		IPR0016020; F:receptor activity; IEA.	
FT	CONFLICT	126	126	Missing (in Ref. 3).		IPR0016020; F:receptor activity; IEA.	
FT	CONFLICT	392	393	KR -> NG (in Ref. 2).		IPR0016020; F:receptor activity; IEA.	
FT	CONFLICT	396	397	RW -> SG (in Ref. 2).		IPR0016020; F:receptor activity; IEA.	
FT	CONFLICT	408	408	A -> R (in Ref. 2).		IPR0016020; F:receptor activity; IEA.	
SEQ	SEQUENCE	431 AA;	49923 MW;	A6D9ED5E75DB8061 CRC64;		KW	
SEQ	SEQUENCE	431 AA;	49406 MW;	63F9C07AFFF5B27 CRC64;		SEQUENCE	428 AA;
Query Match					71.0%;	Score	1582.5;
Best Local Similarity					DB 2;	Length	428;
Matches	26;	Mismatches	29;	Indels	3;	Gaps	2;
Matches	321;	Conservative	26;	Indels	3;	Gaps	2;
Query	38	PEGP- YCSATIDQIGTCWPSLAGEVVERCPDPNSGIRYNTGRVYRECFCENGWTASW	95	Query Match	71.0%;	Score	1582.5;
Db	53	FSGPPTYCNTRLQDQGTCWPQSAQAVLVERCPPEVNGLKNTNTNAVECLENGWTASR	112	Best Local Similarity	73.1%;	Length	428;
Query	96	MNYSQCPVPLDNK-RKAYALYKIALINYIGHC7ISLAIVIAFLFLFLCIRSIRCLRNTH	154	Matches	285;	Conservative	48;
Db	113	VNYSHCEPILDDDKQKDYDHYRALLIVNTYIGHCVSVVALVAFLFLFLVRSIRCLRNTH	172	Indels	5;	Gaps	2;
Query	155	WNLITTFILRNIMWFLQMLDHNTHESNEYWCRCTTINYVYVNTFNMFVEGCVLHTA	214	Query	25	DSFLHSESSSSFFGPEGPYCSATIDQIGTCWPRLAEGELVERCPDPNSGIRYNTGRVY	84
Db	173	WNLITTFILRNIAWFLQLDHEVHEGNBWCRLTTFNQVFMFVEGCVLHTA	232	Db	43	DAANHSDTNN---SGVRCSTVTDGTCWPRLAEGELVERCPDPNSGIRYNTGRVY	98
Query	215	IVMITYSTDKLRKWKVFLFLIGNCIPSPLTIVTWAICKFLYFENEQCWCIGKEPKRYDITYQGRV	274	Query	85	ECPPENGTVWASWNTQSCUPLDNKRYKHYKTAIINLGHGICSLILAVIAFLFLCILR	144
Db	233	IVMITYSTDKLRKWKVFLFLIGNCIPSPLTIVTWAICKFLYFENEQCWCIGKEPKRYDITYQGRV	292	Db	99	KCLANGTWAQPSNYSQCLTAVNQKSKHRYTAIVTINLGHCLSLSTFLTLIAFLFLRLR	158
Query	275	ILVLLINPFLENITVIRLMLKLRASITSETIQYKAVATVLVPLIGTITYMFLFVNQCB	334	Query	145	SIRCIRNTHWNLTTFILRNIMWFLQMLDHNTHESNEYWCRCTTINYVYVNTFNMFVEGCVLHTA	203
Db	293	MLVLLINPFLENITVIRLMLKLRASITSETIQYKAVATVLVPLIGTITYMFLFVNQCB	352	Db	159	SIRCIRNTHWNLTSAFLRNATWFLVQVLTMPDQHESNVPWCLTVTAYNYFMMANFW	218
Query	335	DDVSQIVTFNSFLQSGQFFVSVYCFPLGVEYRVSAAERKRWHDHSLRVVARAMS	394	Query	204	MFVEGCVLHTATIVTYMSTDKLRKWKVFLFLIGNCIPSPLTIVTWAICKFLYFENEQCWCIGKEPKRYDITYQGRV	263
Db	353	DDLSQIVTFNSFLQSGQFFVSVYCFPLGVEYRVSAAERKRWHDHSLRVVARAMS	412	Db	219	MFGCVLHTATIVTYMSTDKLRKWKVFLFLIGNCIPSPLTIVTWAICKFLYFENEQCWCIGKEPKRYDITYQGRV	278
Query	395	IPTSPTRISFSIHKQTAAV	413	Query	264	KYDYYQGRVVLVLYINPFLENIWRILMTKLRASTTSSETIQYKAVATVLVPLIGI	323
Db	413	IPTSPTRISFSIHKQTAAV	431	Db	279	IYDYYQGRVVLVLYINPFLENIWRILMTKLRASTTSSETIQYKAVATVLVPLIGI	338
RESULT 11	Q98UC0	PRELIMINARY;	PRT;	428 AA.	RESULT 12	CRF1_CHICK	STANDARD;
ID	Q98UC0		PRT;	420 AA.	ID	CRF1_CHICK	
AC	Q98UC0;				AC	Q90112;	
DT	01-JUN-2001	(T-TMBLRe1. 17, Created)			DT	01-NOV-1997 (Rel. 35, Created)	
DT	01-JUN-2001	(T-TMBLRe1. 17, Last sequence update)			DT	01-NOV-1997 (Rel. 35, Last sequence update)	
DT	01-MAR-2004	(T-TMBLRe1. 26, Last annotation update)			DT	25-OCT-2004 (Rel. 45, Last annotation update)	
DE	Corticotropin releasing factor receptor 3.				DE	Corticotropin releasing factor receptor 1 precursor (CRF-R) (CRF1)	
OS	Ameiurus nebulosus.				DE	(Corticotropin-releasing hormone receptor 1) (CRH-R 1).	
Organism	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Siluriformes; Ictaluridae; Ameiurus.				OS	Eulinus galius (Chicken).	
OC	Actinopterygii; Neopterygii; Teleostei; Craniata; Vertebrata; Euteleostomi; Ictaluridae; Ameiurus.				OC	Eularyota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Phasianidae; Galliformes; Galliformes; Galliformes.	
OC	Archosauria; Aves; Neognathae; Galliformes; Galliformes.				OC	Archosauria; Aves; Neognathae; Galliformes.	
OC	Galilius.				OC	Galilius.	
[1]	SEQUENCE FROM N.A.				RN	[1] _TaxID=9031;	
RP							

RP	SEQUENCE FROM N.A. PubMed=8536612; DOI=10.1210/en.137.1.192;	Qy	138 LLFLCIRSIRCLRNTHWNLITTFILRNMWFLQCM-IDHNIHESNEWMCRCTTINYF 196
RX	MEIDLINE:96107116; Pubmed=8536612; DOI=10.1210/en.137.1.192;	Db	144 VLFMLRSLTCLRNTHWNLITAFILRNATWVFLNPEHNSVWCLRVAYNF 203
RA	"Molecular cloning of a type A chicken corticotropin-releasing factor receptor with high affinity for urotensin I.";	Qy	197 VVTNFFWMFVEGGCVLHTATVMTYSTDKRKWVFLIGWCIPSPVITWVACKLYVENEQC 256
RT	Endocrinology 137:192-197 (1996).	Db	204 HVTNFFWMFEGGCVLTATVMTYSTDKRKWMFICIGWCIPPFVITWVACKLYVNEKC 263
RL	-!- FUNCTION: this is a receptor for corticotropin releasing factor.	Qy	257 WIGKPGKYDIDYQGRVILVLLNFELENIVRLMLTKURASSTSETIQYRKAKATLV 316
CC	Shows high-affinity binding for urotensin I. The activity of this receptor is mediated by G proteins which activate adenylyl cyclase.	Db	264 WFGKAGVYTDYIYQGRVILVLLNFELENIVRLMLTKURASSTSETIQYRKAKATLV 323
CC	-!- SUBCELLULAR LOCATION: Integral membrane protein.	Qy	317 LLPLIGITMLFFVNPGEVDVSYTIVYFNFSFLQSFGQFFSVYFCFLNGBVRSAAKRW 383
CC	-!- SIMILARITY: Belongs to the G-protein coupled receptor 2 family.	Db	324 LLSLGITYMLFFVNPGEDELSRIVYFNFSFLBSFGQFFSVYFCFLNGBVRSAAKRW 383
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement. (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a> or send an email to license@isb-sib.ch).	Qy	377 HRWQDHSLSLRVVARAMSIPSPTRISPFHKQTAAV 413
CC	DR: L41563; AA:AA96656.1; -.	Db	384 HRWQDHSLSLRVVARAMSIPSPTRISPFHKQTAAV 420
CC	DR: IPR0008; IPK0032; GPCR secretin.	RESULT 13	
CC	DR: InterPro; IPR001879; hormone_receptor.	Q98UC2	PRELIMINARY;
CC	PFam: PF00000; 7tm_2; 1.	ID	Q98UC2
CC	PRINTS: PRO0249; GPCSECRETIN.	AC	Q98UC2;
CC	SMART: SM00008; HormP; 1.	DT	01-JUN-2001 (TREMBLrel. 17, Created)
CC	PROSITE: PS00649; G PROTEIN RECBP F2; 1.	DT	01-JUN-2001 (TREMBLrel. 17, Last sequence update)
CC	DR: PROSITE: PS00650; G PROTEIN RECBP F2; 2; 1.	DT	01-MAR-2004 (TREMBLrel. 26, Last annotation update)
CC	DR: PROSITE: PS5037; G PROTEIN RECBP F2; 3; 1.	DR	Corticotropin releasing factor receptor 1.
CC	DR: PROSITE: PS50261; G PROTEIN RECBP F2; 4; 1.	DR	Ameiurus nebulosus.
CC	KW G-protein coupled receptor; Gycoprotein; Signal; Transmembrane.	DR	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Siluriformes; Actinuridae; Ameiurus.
CC	FT SIGNAL 1 28	DR	NCBI_TaxID=27778;
CC	FT CHAIN 29 420	OX	NCBI_TaxID=27778;
CC	1. G-protein coupled receptor receptor	RN	
FT	1. Corticotropin releasing factor receptor	RP	
FT	1. Extracellular (Potential).	SEQUENCE FROM N.A.	
FT	1. (Potential).	MEDLINE=21066341; PubMed=11145609; DOI=10.1210/en.142.1.446;	
FT	1. Cytoplasmic (Potential).	RX	
FT	2. (Potential).	RA	
FT	2. Extracellular (Potential).	RT	
FT	3. (Potential).	RT	"Characterization of three corticotropin-releasing factor receptors in catfish: a novel third receptor is predominantly expressed in pituitary and urophysis",
FT	3. Cytoplasmic (Potential).	RT	Endocrinology 142:446-454 (2001).
FT	4. (Potential).	RL	AF223359; AAC01068.1; -.
FT	4. Extracellular (Potential).	DR	GO; GO:0016030; F:G-Protein coupled receptor activity; IEA.
FT	5. (Potential).	DR	GO; GO:0004872; F:receptor activity; IEA.
FT	5. Cytoplasmic (Potential).	DR	InterPro; IPR01052; CRP1 receptor.
FT	6. (Potential).	DR	InterPro; IPR003051; CRF receptor.
FT	6. Extracellular (Potential).	DR	InterPro; IPR000832; GPCR secretin.
FT	7. (Potential).	DR	InterPro; IPR001879; hormone_receptor.
FT	7. Cytoplasmic (Potential).	DR	Pfam; PF00002; 7tm_2; 1.
FT	By Similarity.	DR	Pfam; PF02793; Horm; 1.
FT	By similarity.	DR	PRINTS; PRO1279; CRPRECEPTOR.
FT	By similarity.	DR	PRINTS; PRO1280; CRPRECEPTOR.
FT	73 107	DR	PRINTS; PRO0249; GPCRECRETIN.
FT	N-linked (GICNAC. . .) (Potential).	DR	SMART; SM00008; HormR; 1.
FT	N-linked (GICNAC. . .) (Potential).	DR	PROSITE; PS00650; G PROTEIN RECBP F2; 1; UNKNOWN_1.
FT	N-linked (GICNAC. . .) (Potential).	DR	PROSITE; PS00650; G PROTEIN RECBP F2; 2; 1.
FT	N-linked (GICNAC. . .) (Potential).	DR	PROSITE; PS50227; G PROTEIN RECBP F2; 3; 1.
FT	N-linked (GICNAC. . .) (Potential).	DR	PROSITE; PS50261; G PROTEIN RECBP F2; 4; 1.
SQ	SEQUENCE 420 AA; 48600 MW;	SEQUENCE	445 AA; 51062 MW; F17DA70BB22BB755 CRC64;
CC	Score 1582; DB 1; Length 420;	Query Match	Score 1578.5; DB 2; Length 445;
CC	Best Local Similarity 72.3%; Matches 49; Mismatches 55; Indels 6; Gaps 2;	Best Local Similarity	70.8%; Mismatches 39; Indels 48; Gaps 1;
CC	287; Conservative	Matches	76.5%; Pred. No. 2 6e-109;
Qy	18 SLLDAFDQFLHSRSSTSSFFGEGYCSCATIDQIGTCNPRSLAGELVPRCPDSFGNIRYNTTRVYRECFCFGNTWASNNYNS 99	287; Conservative	39; Mismatches 48; Indels 1; Gaps 1;
Db	29 SIOQYCESSLPLPTNHT-----GFOQNAASVLDLGTWRSAYCQLVAPCPPEFYGRYN 83	Qy	40 GPCYSARIQDQIGTCWPRSLAGELVPRCPDSFGNIRYNTTRVYRECFCFGNTWASNNYNS 99
Qy	78 TTRVYREPFENGTWASNNYSSQCVPIILDKRKYALHCKIALIINVLGHCISLALVIAF 137	Db	71 GLFCNTISDGTCTCWPNSNAGITVSRCPCPETLGVRNTTNNVYRECFCFGNTWASNNYNS 130
Db	84 TTNGYRECLANGSWAARTVNSQCEQELSEEKSKLHThIAVINYLGCVSLGTLVIAF 143	Qy	100 QCVPLDNKRYALHCKIALIINVLGHCISLALVIAFLLFLCLRSIRCLANHNLIT 159

Db	131	QCQEINNEBEKSKLHYHIAVINYLGHCISIGALLIVAFILFMRLMIRCLRNITHWNLLM	190	Qy	141	LCRSIRCLRNITHWNLLTTFILRNIMMFLQOM-IDRNTHESNEWWCRCITIYNYFVTT	199
Qy	160	TFILRNIMMFLQOM-IDRNTHESNEWWCRCITIYNYFVTTNEFMPVFGCILHATVMT	218	Db	142	LRLSIRCLRNITHWNLLSAFLRNATWVQJMSPEPHQSANGWCRLVTAAYNYFVTT	201
Db	191	AFLRNATWVQJLTMNPVEHESVWCRLVTAATNYFVTTNEFMPVFGCILHATVMT	250	Qy	200	NFFMFVFGCYLHTAIVMITYSTDKLRKVNVLFLFGCIPSPPIVTTWACKLYFENQKCWIG	259
Qy	219	YSTDKLRKVNVLFLFGCIPSPPIVTTWACKLYFENQKCWIGKEPERIYDYGCRVLVL	278	Db	202	NFFMFVFGCYLHTAIVMITYSTDKLRKVNVLFLFGCIPSPPIVTTWACKLYFENQKCWIG	261
Db	251	YSTDKLRKVNVLFLFGCIPSPPIVTTWACKLYFENQKCWIGKEPERIYDYGCRVLVL	310	Qy	260	KEPGYIDYIYQGRVILVLLNFVFLNVRIMTKLRASTTSETIQRKAVAKATVLVLPP	319
Qy	279	LINFVFLNVRIMTKLRASTTSETIQRKAVAKATVLVLPLGIGTMYLFFVNPGEDDVS	338	Db	262	KRPGYTDIYQGPMLVLLNFVFLNVRIMTKLRASTTSETIQRKAVAKATVLVLPP	321
Db	311	LINFVFLNVRIMTKLRASTTSETIQRKAVAKATVLVLPLGIGTMYLFFVNPGEDDVS	370	Qy	320	LLGTYMLFFVNPGEDDVSQGIVFVYFNSTLQSIVFVYFNSTLQSIVFVYFNSTLQSIV	379
Qy	339	QIVFVYFNSTLQSIVFVYFNSTLQSIVFVYFNSTLQSIVFVYFNSTLQSIVFVYFNSTLQSIV	398	Db	322	LGTYMLFFVNPGEDDVSQGIVFVYFNSTLQSIVFVYFNSTLQSIVFVYFNSTLQSIV	381
Db	371	QIVFVYFNSTLQSIVFVYFNSTLQSIVFVYFNSTLQSIVFVYFNSTLQSIVFVYFNSTLQSIV	430	Qy	380	QDHHSIRVYVARANSIPTSPTRISFSHKQTAAY	413
Qy	399	PTRISFSHSIKQTAAY	413	Db	382	QDKHSIRVYVARANSIPTSPTRISFSHKQSTAV	415
Db	431	PTRVSFHSIKQSSAV	445				
RESULT 14							
Q7 6LL8		PRELIMINARY;		PRT;	415	AA.	
ID	Q76LL8						
AC	Q76LL8;						
DT	05-JUL-2004	(TREMBL)rel. 27. Created)					
DT	05-JUL-2004	(TREMBL)rel. 27. Last sequence update)					
DT	05-JUL-2004	(TREMBL)rel. 27. Last annotation update)					
DB		Corticotropin releasing factor receptor type 1.					
GN	Name=CRF1;						
OS	Xenopus laevis (African clawed frog)						
OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;						
OC	Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;						
OC	Cercopithecoidea; Macaca.						
NCBI_TaxID	9544;						
RN	[1]						
RP	SEQUENCE FROM N.A.						
RA	Oshida Y., Ikeda Y., Chaki S., Okuyama S.;						
RL	Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.						
DR	EMBID: AB078141; BAD02831.1; -						
DR	GO: GO:0016020; C:membrane; IBA.						
GO	GO:0004930; F:G-protein coupled receptor activity; IEA.						
DR	GO: GO:0004872; F:receptor activity; IER.						
DR	InterPro; IPR003052; CRF receptor.						
InterPro	IPR003051; CRF receptor.						
DR	InterPro; IPR000832; GPCR secretin.						
DR	InterPro; IPR001879; hormn_receptor.						
Pfam	Pf00002; 7tm_2; 1.						
DR	Pfam; PF02793; HRM_1;						
PRINTS	PR01279; CRPRECEPTOR.						
DR	PR01280; CRPRESECRETOR.						
SMART	SM00008; Hormn; 1.						
PROSITE	PS00619; G PROTEIN RECEP F2_1; 1.						
DR	PROSITE; PS00650; G PROTEIN RECEP F2_2; 1.						
DR	PROSITE; PS50227; G PROTEIN RECEP _F2_3; 1.						
DR	PROSITE; PS50251; G PROTEIN RECEP _F2_4; 1.						
KW	Receptor.						
SEQUENCE	415 AA;	47784 MW;	84C530DEC6DA97AD CRC64;				
Query Match	70-3%;	Score 1566;	DB 2;	Length 415;			
Best Local Similarity	72.8%;	Pred. No. 2.1e-108;					
Matches	287;	Conservative	46;	Mismatches 57;	Indels 4;	Gaps 3;	
Db	24	AFQDSFLHSESSSS-FGEFGPYCSATIDQIGTCMPSLAGELVERRPCDPSNGRYNTTR	80				
Qy	22	AFQDSFLHSESSSS-FGEFGPYCSATIDQIGTCMPSLAGELVERRPCDPSNGRYNTTR	80				
Db	24	SLQDQ-HCELSLNLASNLNQCNASVQDLSLTCWPSLQVRPCPAPFYGRYNTTR	81				
Qy	81	NYRECPEGTWASWNYSQCVPLDNRKRYALHYKIALINYLGHCISSLALVIAFLF	140				
Db	82	NGYRECANGSWAARVNYSECOELNEEKSKVHYVAVINYLGHCISLVALVAVFLF	141				

FT SIGNAL 1 24 Potential.  
 FT CHAIN 25 415 Corticotropin releasing factor receptor  
 FT DOMAIN 25 121 Extracellular (Potential).  
 FT TRANSMEM 122 142 1 (Potential).  
 FT DOMAIN 143 151 Cytoplasmic (Potential).  
 FT TRANSMEM 152 171 2 (Potential).  
 FT DOMAIN 172 189 Extracellular (Potential).  
 FT TRANSMEM 190 213 3 (Potential).  
 FT DOMAIN 214 227 Cytoplasmic (Potential).  
 FT TRANSMEM 228 249 4 (Potential).  
 FT DOMAIN 250 268 Extracellular (Potential).  
 FT TRANSMEM 269 291 5 (Potential).  
 FT DOMAIN 292 314 Cytoplasmic (Potential).  
 FT TRANSMEM 315 334 6 (Potential).  
 FT DOMAIN 335 349 Extracellular (Potential).  
 FT TRANSMEM 350 369 7 (Potential).  
 FT DOMAIN 370 415 Cytoplasmic (Potential).  
 FT DISULFID 30 54 By similarity.  
 FT DISULFID 44 87 By similarity.  
 FT DISULFID 68 102 By similarity.  
 FT CARBOHYD 38 38 N-linked (GLCNAC. .) (Potential).  
 FT CARBOHYD 45 45 N-linked (GLCNAC. .) (Potential).  
 FT CARBOHYD 78 78 N-linked (GLCNAC. .) (Potential).  
 FT CARBOHYD 90 90 N-linked (GLCNAC. .) (Potential).  
 SQ SEQUENCE 415 AA; 47786 MW; 74ED24C17907B74D CRC64;

Query Match 70.2%; Score 1564.5; DB 1; Length 415;  
 Best Local Similarity 72.2%; Pred. No. 2.7e-108;  
 Matches 285; Conservative 49; Mismatches 58; Indels 3; Gaps 2;

Qy 20 LDAFDQDSFLHSSSSSSFGFEGPYCSATTIDQIGTCWPRSLAGEVLVERPCDSENGTRYNTT 79  
 Db 23 L7SLQDQETL0NS--NFTGLACNASTDMIGCWPSSTAQGMVAPCPETFHGQYNTT 80

Qy 80 RNVYRECENGFTWASWNNYNSOCYVPLIDNKRKYALHYKIALINYLGHCSISITALVIAFLL 139  
 Db 81 GNVYRECCHLNGSWAGRGDPAQCOEILKQEKCTKHYTAIVNFGHSISCALLVAFIL 140

Qy 140 FLCRLSIRCLRNTHWNLITITLRLNMWFLQM-IDHNIHESNEWCRCTTIVNYFVV 198  
 Db 141 FLRLSIRCLRNTHWNLITATLRLNWTWYQWQLTLSHEARDNSVWCRLVTTIANYFVV 200

Qy 159 TNFFWMFVEGCTYHTATWMTYSTDKLKRKWFELFIGWCLPSPLIVTAICLKLYENFQCIWI 258  
 Db 201 TNFFWMFEGCTYHTATLVLTYSTDKLKRKWFELFIGWCLPSPLIVTAICLKLYENFQCIWI 260

Qy 259 GKEPGKYIDYIYQGRVILLINFEVLNIVRLMTKRASTSETIQYRKAVAKTLL 318  
 Db 261 GKEAGVYTDIYQGPVILVLLNIFLNLVRLMTKRASTSETIQYRKAVAKTLL 320

Qy 319 PLIGITMLPFPNGPQEDVSQVPIYFNSFLQSFQGPVSVYPCFNGEVSAARKRWR 378  
 Db 321 PLIGITMLPFPGEDEISRIVFVYFQGPVSVYPCFLNSEVRSAVRKRWR 380

Qy 379 WQDHHSLRVRAVAMSIPTSPTRISFHIKQTAAV 413  
 Db 381 WQDKHSIRARVARAMSISPTSPTRISFHISQSSAI 415

Search completed: August 20, 2005, 00:28:25  
 Job time : 171 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 20, 2005, 00:18:48 ; Search time 40 Seconds  
(without alignments)  
993.438 Million cell updates/sec

Title: US-10-649-852-32

Perfect score: 2229

Sequence: 1 MDSTIFELIIDEFDANGSSL.....SIPTSPTRISFSIKOTAAV 413

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing First 45 summaries

Database : PIR79:  
1: pir1:  
2: pir2:  
3: pir3:  
4: pir4:  
4:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	% Length	DB ID	Description
1	1793	80.4	411	2 A5610	corticotropin-rele
2	1770.5	79.4	431	2 I4519	CRF receptor - mou
3	1769	79.4	430	2 A56726	corticoliberin rec
4	1746.5	78.4	431	2 I44279	sauvagine/corticot
5	1554.5	69.8	415	2 S3535	corticotropin-rele
6	1551.5	69.6	415	2 I58144	corticotropin-rele
7	1511.5	69.2	444	2 A42260	corticoliberin rec
8	1408.5	63.2	375	2 A38879	corticotropin-rele
9	612	27.5	585	2 A3286	parathyroid hormon
10	595.5	26.7	479	2 S33746	calcitonin receptor
11	593	26.6	515	2 I49154	calcitonin receptor
12	590	26.5	515	2 I60800	calcitonin receptor
13	588.5	26.4	478	2 A37430	calcitonin receptor
14	588.5	26.4	593	2 A49191	parathyroid hormon
15	587	26.3	474	2 I37217	calcitonin receptor
16	569	25.5	490	2 S34486	parathyroid hormon
17	567	25.4	591	2 I54195	parathyroid hormon
18	565.5	25.4	591	2 S44203	calcitonin receptor
19	556.5	25.3	482	2 A32985	secretin receptor
20	555.5	24.8	449	2 S16319	calcitonin-like re
21	551.5	24.8	464	2 I60194	secretin receptor
22	553	24.8	440	2 JC2532	calcitonin receptor
23	544.5	24.6	461	2 JC2477	calcitonin receptor
24	546	24.5	498	2 I47130	parathyroid hormon
25	545	24.5	589	2 I59297	parathyroid hormon
26	535.5	24.0	550	2 A57519	vasoactive intesti
27	516.5	23.2	459	2 JH0594	vasoactive intesti
28	506	22.7	460	2 JC2194	glucose-dependent
29	506	22.7	495	2 JC2195	glucose-dependent

## ALIGNMENTS

RESULT 1

AS5610 corticotropin-releasing factor receptor subtype 2 - rat

C;Species: Rattus norvegicus (Norway rat)

C;Date: 02-Jul-1996 #sequence\_change 09-Jul-2004

C;Accession: A55610

R;Loverberg, T.W.; Liaw, C.W.; Grigoriadis, D.E.; Clevenger, W.; Chalmers, D.T.; De Souz Proc. Natl. Acad. Sci. U.S.A. 92, 836-840, 1995

A;Title: Cloning and characterization of a functionally distinct corticotropin-releasing A;Reference number: A55610; PMID:95148632; PMID:846062

A;Status: Preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Cross-references: UNIPROT:P47866; EMBL:U16253; PID:9644771; PID:9644771; PID:96447

C;Genetic:

C;Gene: CRF2R

C;Superfamily: Glucagon receptor

Query Match 80.4%; Score 1793; DB 2; Length 411;

Best Local Similarity 80.0%; Pred. No. 9.4e-143;

Matches 333; Conservative 30; Mismatches 45; Indels 8; Gaps 4;

QY 1 MDSTFELIIDEFDANSCLLDAFQDSFLHSESSSSFFEGGP--YSSATIDQIGTQPRSL 58

1 MDAA---LLSLLLEANCSL--ALAEBLLLQWGEPPDPEPDSYCNNTLQIGTCMPQSA 55

QY 59 AGELYVERPCDPSENGTRNTTRVYRECFCNGTWSAWMNTSQCVPLDNK-RKVALHYK 117

56 PGALVERPCPXYENGKQYNTNTNARECLNGTWSRINSHCCEPLDQKRYDQKHYR 115

QY 118 ALIINNLGHCSILILAVIAFLFLCLRSIRCLRNTHWNLITTFIRNIMWFLQGMIDHN 177

116 ALIINNLGHCSVVAFLFLVLRSTRLRNTHWNLITTFIRNNTWFLQJLIDHE 175

QY 178 IHESNWWRCCITTYIINYFVVTNFWMFVEGCVLTTAIVNTYSTDLKRKUVFLFGWCIP 237

176 VHEGNEWWRCCVTTIINYFVVTNFWMFVEGCVLTTAIVNTYSTDLKRKUVFLFGWCIP 235

QY 238 SPIIVTWAICKLFLYNEBQCNIGKEPKSYIDYIYQGRVILVLLINPVFLNTRILMTKL 297

236 CPIIVAWAVGRLYYNEBQCNIGKEPKSYIDYIYQGRVILVLLINPVFLNTRILMTKL 295

QY 298 ASTTSETIQKAVKATVLLPLLGLITMFLFVNQGDDYQIVFIVYENSPFLQSGQFFV 357

296 ASTTSETIQKAVKATVLLPLLGLITMFLFVNQGDDYQIVFIVYENSPFLQSGQFFV 355

QY 358 SVFYCFNGEYRSAAKRKRWQDHISLRVVARAAMSISPTSPTRSFHSIKQTAAV 413

Db 356 SVFYCFNGEYRSAAKRKRWQDHISLRVVARAAMSISPTSPTRSFHSIKQTAAV 411



Qy	395 IPTSPRISFSIKQTAAN 413	Query Match 69.6%; Score 1551.5; DB 2; Length 415;
Db	413 IPTSPRISFSIKQTAAN 431	Best Local Similarity 74.7%; Pred. No. 1.7e-122; Mismatches 50; Indels 1; Gaps 1;
RESULT 5		
S3 9535	corticotropicin-releasing hormone receptor - mouse	
C;Species: Mus musculus (house mouse)		
C;Date: 01-Oct-1994 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004		
R;Accession: S3 9535		
R;Vita, N.; Laurent, P.; Lefort, S.; Chalon, P.; Lelias, J.M.; Kaghad, M.; le Fur, G.; PBS Lett. 335, 1-5, 1993		
A;Title: Primary structure and functional expression of mouse pituitary and human brain		
A;Reference number: S3 9534; MUID:90063063; PMID:8243652		
A;Accession: S3 9535		
A;Status: preliminary		
A;Molecule type: mRNA		
A;Residues: 1-415 <VIT>		
A;Cross-references: UNIPROT:P35347; EMBL:X72305; NID:9436120; PIDN:CAA51053.1; PID:94361		
A;Note: the sequence from Fig. 1 is inconsistent with that from Fig. 3 in having an addi		
C;Superfamily: Glucagon receptor		
C;Keywords: G protein-coupled receptor; transmembrane protein		
Query Match 69.8%; Score 1556.5%; DB 2; Length 415;		
Best Local Similarity 74.9%; Pred. No. 6.4e-123; Mismatches 44; Indels 1; Gaps 1;		
Matches 281; Conservative 44; Mismatches 49; Indels 1; Gaps 1;		
Db	40 GPYCSATIDQIGTCWPSLAGEVLPFCDSNGTRNVTNRECFENGTRWASWVNYS 99	Qy 339 QIVFVYENSPLOSGFQFVSYVCFINGEVYRSAARKRWRQDHSLRVVARANSIPTS 398
Db	41 GLQCNASVDSLIGTCWPSAGLVVRPCPAFFYGRYNTNTNGRECLANGSWARVNYS 100	Db 279 LINFVFLFVNIVRLMTKLRASTSTIQRKAVATLVLPLGLTYMLFVNPODEDEVS 338
Qy	100 QCVPLIDNKRKYAHYKIALINYLGHCSISLALVTAFLFLCLRSIRCLRNTHWNLIT 159	Db 281 LINFVFLFVNIVRLMTKLRASTSTIQRKAVATLVLPLGLTYMLFVNPODEDEVS 340
Db	101 ECQEELNEEKGSVKVHAYAVINLYLGHCSISLALVTAFLFLCLRSIRCLRNTHWNLIS 160	RESULT 7
Qy	160 TPFLRNIMWFLQI-IDNTHNESNEWCRCTTIVNYFVUTNPFMVEGGYLTAIVMT 218	A48260 corticoliberin receptor, long splice form - human
Db	161 APFLRNATWFLVFLQIPEVOSVNAWRLVTAATVNYFVUTNPFMVEGGYLTAIVLT 220	N;Alternative names: corticotropin releasing factor receptor
Qy	162 QIVFVYENSPLOSGFQFVSYVCFINGEVYRSAARKRWRQDHSLRVVARANSIPTS 398	C;Species: Homo sapiens (man)
Db	163 QIVFVYENSPLOSGFQFVSYVCFINGEVYRSAARKRWRQDHSLRVVARANSIPTS 398	C;Date: 31-May-1996 #sequence_revision 11-Apr-1997 #text_change 09-Jul-2004
Qy	164 QIVFVYENSPLOSGFQFVSYVCFINGEVYRSAARKRWRQDHSLRVVARANSIPTS 398	R;Chan, R.; Lewis, K.A.; Perrin, M.H.; Vale, W.W.
Db	165 QIVFVYENSPLOSGFQFVSYVCFINGEVYRSAARKRWRQDHSLRVVARANSIPTS 398	Proc. Natl. Acad. Sci. U.S.A. 90, 8967-8971, 1993
Qy	166 QIVFVYENSPLOSGFQFVSYVCFINGEVYRSAARKRWRQDHSLRVVARANSIPTS 398	A;Title: Expression cloning of human corticotropin-releasing factor (CRF) receptor.
Db	167 QIVFVYENSPLOSGFQFVSYVCFINGEVYRSAARKRWRQDHSLRVVARANSIPTS 398	A;Reference number: A48260; MUID:94022996; PMID:7692441
Qy	168 QIVFVYENSPLOSGFQFVSYVCFINGEVYRSAARKRWRQDHSLRVVARANSIPTS 398	A;Accession: I60975
Db	169 QIVFVYENSPLOSGFQFVSYVCFINGEVYRSAARKRWRQDHSLRVVARANSIPTS 398	A;Status: translated from GB/EMBL/DBJ
Qy	170 QIVFVYENSPLOSGFQFVSYVCFINGEVYRSAARKRWRQDHSLRVVARANSIPTS 398	A;Molecule type: mRNA
Db	171 QIVFVYENSPLOSGFQFVSYVCFINGEVYRSAARKRWRQDHSLRVVARANSIPTS 398	A;Residues: 1-444 <RES>
Qy	172 QIVFVYENSPLOSGFQFVSYVCFINGEVYRSAARKRWRQDHSLRVVARANSIPTS 398	A;Cross-references: UNIPROT:P34998; GB:L23333; NID:9408691; PIDN:AAA35719.1; PID:9408692
Db	173 QIVFVYENSPLOSGFQFVSYVCFINGEVYRSAARKRWRQDHSLRVVARANSIPTS 398	A;Experimental source: Cushing corticotropin cell tumor
Qy	174 QIVFVYENSPLOSGFQFVSYVCFINGEVYRSAARKRWRQDHSLRVVARANSIPTS 398	A;Accession: A48260
Db	175 QIVFVYENSPLOSGFQFVSYVCFINGEVYRSAARKRWRQDHSLRVVARANSIPTS 398	A;Status: preliminary; translated from GB/EMBL/DBJ
Qy	176 QIVFVYENSPLOSGFQFVSYVCFINGEVYRSAARKRWRQDHSLRVVARANSIPTS 398	A;Molecule type: mRNA
Db	177 QIVFVYENSPLOSGFQFVSYVCFINGEVYRSAARKRWRQDHSLRVVARANSIPTS 398	A;Residues: 1-145-175-444 <RES2>
Qy	178 QIVFVYENSPLOSGFQFVSYVCFINGEVYRSAARKRWRQDHSLRVVARANSIPTS 398	A;Cross-references: GB:L23332; NID:9408689; PIDN:CAA51052.1; PID:9436119
Db	179 QIVFVYENSPLOSGFQFVSYVCFINGEVYRSAARKRWRQDHSLRVVARANSIPTS 398	A;Note: the sequence from Fig. 1 is inconsistent with that from Fig. 3 in having an add.
Qy	180 QIVFVYENSPLOSGFQFVSYVCFINGEVYRSAARKRWRQDHSLRVVARANSIPTS 398	C;Genetics:
Db	181 QIVFVYENSPLOSGFQFVSYVCFINGEVYRSAARKRWRQDHSLRVVARANSIPTS 398	A;Gene: CRHR1; CRHR; CRF-R; CRF1
RESULT 6		A;Cross-references: GDB:35922; OMIM:122561
158144	corticotropicin-releasing factor receptor - rat	A;Map position: 17q12-17q22
C;Species: Rattus norvegicus (Norway rat)		C;Superfamily: Glucagon receptor
C;Accession: T58144		C;Keywords: alternative splicing; transmembrane protein
R;Chang, C.P.; Pearce, R.V.; O'Connell, S.; Rosenfeld, M.G.		C;Cross-references: UNIPROT:P35353; GB:L25438; NID:9450298; PIDN:AAA16441.1; PID:9457615
A;Title: Identification of a seven transmembrane helix receptor for corticotropin-releas		
A;Reference number: 158144; MUID:9409969; PMID:8224282		
A;Accession: T58144		
A;Status: preliminary; translated from GB/EMBL/DBJ		
A;Molecule type: mRNA		
A;Residues: 1-415 <RES>		
A;Cross-references: UNIPROT:Q09969		
C;Superfamily: glucagon receptor		
C;Keywords: alternative splicing; transmembrane protein		

Query Match	69.2%	Score 1541.5;	DB 2;	Length 444;	Qy	316 VLLPLGLITYMLPFVNPGEDDVSQIVFVNSPLQSGFVFSVFCPLNGEVRSARKR	375
Best Local Similarity	67.8%	Pred. No. 1.2e-121;					
Matches	287;	Conservative	46;	Mismatches	57;	Indels	33;
							Gaps 4;
Qy	22 AFQDFSLHSSSSF-FGFEPPYC SATIDQIGTCWPSLAGELYVERCPDPSFNGIRYNTF 80				Db	278 VLLPLGLITYMLPFVNPGEDDVSQIVFVNSPLQSGFVFSVFCPLNGEVRSARKR	337
Db	24 SLQDQ-HCESSLASLNISGLQCNASVDLIGTCWPSLGPQLVVRCPDPSFNGIRYNTF 81				Qy	376 WHRQDHSLSLRVYVARAMS ITPSPTRISFHSIKOTAAV	413
Qy	81 NVRSCFENGTWASWMMYSCVCPILDNKRYKALIINYLGHCIISLALVIAFLR 140				Db	338 WHRQDHSLSLRVYVARAMS ITPSPTRISFHSIKOTAAV	375
Db	82 NGYRECLANSWAARVNYSCQELNEECKSKVHYAVLNVLGHCIISLALVIAFLR 141						
Qy	141 LCL-----RSERCLNLIHWNLITFLNIMWFL 171						RESULT 9
Db	142 IRLRGCFCTHGDQADGALIYVAPMSGA PFOVRSTRCLNIIHWNLISFLERNATWVY 201						
Qy	172 QM-IDHNIHESNEWCRCTTINYFVVTNFWMFVEGGCYLHTATVMTSTDKLRKWFV 23.0						
Db	202 QLMSPSEVHQVNMGCRVLAAYNPHVNTFWMFEGGCYLHTATVLTSTDKLRKWFV 261						
Qy	231 FIGWCUPSPVLTWMAKLYYENECOCWIGKEPGKHDYIYQGRVTLVLLINFEVFLNVR 290						
Db	262 CIGWGVPPFTIVAWAIGKLYYDNERCXWFGSRGPYTTDYYQGPMTLVLINFEVFLNVR 321						
Qy	291 ILMTKRERASSETSETIQRKRAVKATLVLLPLGLITYMLPFVNPGEDDVSQIVFVNSFLQ 350						
Db	322 ILMTKRERASSETSETIQRKRAVKATLVLLPLGLITYMLPFVNPGEDDVSQIVFVNSFLQ 381						
Qy	351 SFQGFPEVSFVFCPLNGEVRSARKWHRDHSLSLRVYVARAMS ITPSPTRISFHSIKOT 41.0						
Db	382 SFQGFPEVSFVFCPLNSEVRSARKWHRDHSLSLRVYVARAMS ITPSPTRISFHSIKOT 441						
Qy	411 AAV 413						
Db	442 TAV 444						
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C;Species: Homo sapiens (man)							
C;Date: 29-May-1998	#sequence_revision 29-May-1998	#text_change 09-Jul-2004					
C;Accession: 138879							
R;Ross, P. C.; Kostas, C.M.; Ramabhadran, T.V.							
BioChem, Biophys. Res. Commun. 205, 1836-1842, 1994							
A;Title: A variant of the human corticotropin-releasing factor (CRF) receptor: cloning, translation, and expression							
A;Accession: 138879							
A;Status: preliminary; translated from GB/EMBL/DDBJ							
A;Residue: 1-375 <RES>							
A;Cross-references: UNIPROT:P24998;							
C;SuperFamily: Glucagon receptor							
Query Match	63.2%	Score 1408.5;	DB 2;	Length 375;	Qy	308 RAKVLTQVPLGKTYMLFVNLQFSEKYLWGLTFLWNGLPAVFWVVTBTRAT	339
Best Local Similarity	75.4%	Pred. No. 1.5e-110;					
Matches	255;	Conservative	41;	Mismatches	41;	Indels	1;
							Gaps 1;
Qy	77 NTTRVNYRECPENGTWASWMMYSCVCPILDNKRYKALIINYLGHCIISLALVIA 136				Qy	365 NGEVYRSAARKWHRW 379	
Db	38 NISDNGYRECLANGSWAARVNYSECQELNEEKSKVHVAVINYLGHCIISLALVIA 97				Db	457 NGEVQAEIKKWSRW 471	
RESULT 10							
Qy	137 FLLFLCLRSIRCLNLIHWNLITFLNIMWFLQ-M-IDHNTESNEYWCRCTTINYX 195						
Db	98 FVLFRLRSIRCLNLIHWNLISAFLRLNATWVFLQTLTSPVEHSNVWCRLWTAANY 157						
Qy	196 FVVTNFWMFVEGGCYLHTATVMTSTDKLRKWFVYPLGKTYMLFVNLQFSEKYLWGLTFLWNGLPAVFWVVTBTRAT						
Db	158 FVVTNFWMFVEGGCYLHTATVMTSTDKLRKWFVYPLGKTYMLFVNLQFSEKYLWGLTFLWNGLPAVFWVVTBTRAT						
Qy	256 CWIGRPKGKYIDYNGRVLVLLNFENIWRILMFLKRASTTSETIQYRKAVATL 315						
Db	218 CWFGKRPGVYTDY-TQGPMLVLLNFENIWRILMFLKRASTTSETIQYRKAVATL 277						





A;Title: Cloning and characterization of an abundant subtype of the human calcitonin receptor  
 A;Reference number: 137217; MUID:93359437; PMID:8078488  
 A;Accession: 137217  
 A;Status: preliminary; translated from GB/EMBL/DBJ  
 A;Molecule type: mRNA  
 A;Residues: 1-474 <RES>  
 A;Cross-references: EMBL:X69920; NID:9474931; PID:CAA49541.1; PID:9474932  
 R; Frendo, J.-L.; Pichaud, P.; Delage Mouroux, R.; Bouizar, Z.; Segond, N.; Moukhtar, M.S  
 FEBS Lett. 342, 214-216, 1994  
 A;Title: An isoform of the human calcitonin receptor is expressed in TT cells and in med  
 A;Reference number: S43673; MUID:94192834; PMID:8143880  
 A;Accession: S43673  
 A;Molecule type: mRNA  
 A;Residues: 121-168, 'X', 170-199, 'X', 201-216 <FRE>  
 C;Genetics:  
 A;Gene: GDB: CALCR  
 A;Cross-references: GDB:138127; OMIM:114131  
 A;Map position: 7q21.3-7q21.3  
 C;Superfamily: glucagon receptor  
 C;Keywords: transmembrane protein

Query Match 26.3%; Score 587; DB 2; Length 474;  
 Best Local Similarity 34.3%; Pred. No. 1.4e-11;  
 Matches 137; Conservative 73; Mismatches 151; Indels 38; Gaps 14;

Qy	19	LIDAFQDSFLHSESSSPFGFEGPYCSATIDQIGTCMPSRLAGELVERPCPDSFNGTRYNT 78
Db	48	MMDAQKYCDRNMQLPAVQGEGYCNRWDG-WLCWDDTPAGVLSYQFCPDYFPD-FDP 104
Qy	79	TRNVYRECENGTV-----ASWMNYSQCYPILDNKRK-YALHYKIALTINYLGHCIS 129
Db	105	SEKVTYKCDKEGWFKHDEENRTWSNTMCNAFTPEKLKNAYVLY-LATV---GHSLS 159
Qy	130	ILALVIAFLFLFLCLRSIRCLANLHNMLITPLRNIMWFLQIMD--HNTHESNEVW 185
Db	160	IFTLVIISGIVYFVRSIGCQRTVTLHKNMFLTYL-NSMIIILHLLVEVVPENGELVRRDPVS 218
Qy	186	CRGTTTNYFVYTFNFMFVERGTYLTATIYVMTDRLR-KWVFLPFGWCLPSPLIVTW 244
Db	219	CKLHPPFFQMMACNYFMLCGLGIVLHLLIVAVFTEKQLRWWYL LGWGPLVPTIH 277
Qy	245	AICKLFYFNEQCWIGKEPGKTYDIIYQGRVILVLLINFVFLNIVRILMTKLRASTTSET 304
Db	278	ATRAVYFENDNCWLSV-E-THLILYINGPVMALVWNFFLNVRLVTKMRETHEAS 335
Qy	305	IQYRKAVATLVLPLIGITYMLFFNNGEDDVSOIYTFYENFSFLQSGFQFVSVFPCFL 364
Db	336	HMYLKAVATMILVPLJQFVVFPMRFSNKMGLGKI-YDYMWHSLTHFQGPFVATIYFC 394
Qy	365	NGEVRSARKRW-----HFW---QDHHSJRVVARA 392
Db	395	NNEVQTTVKRQWAQFKTQWNRGRPSNRSARAAAAA 433

Search completed: August 20, 2005, 00:29:10  
 Job time : 41 secs

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GenCore version 5.1.6

OM protein - protein search, using SW model

Run on: August 20, 2005, 00:28:34 ; Search time 163 Seconds

952.178 Million cell updates/sec (without alignments)

Sequence: 1 MDSTIFETIIDEFDANCSLL.....SIPTSPTRISFSIKTAAV 413

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1759131 seqs, 391586102 residues

Total number of hits satisfying chosen parameters: 1759131

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Published Applications AA:\*

1: /cgn2\_6/ptodata/2/pubcaa/US07\_PUBCOMB.pep:\*

2: /cgn2\_6/ptodata/2/pubcaa/US06\_NEW\_PUB.PEP:\*

3: /cgn2\_6/ptodata/2/pubcaa/US06\_PUBCOMB.pep:\*

4: /cgn2\_6/ptodata/2/pubcaa/US06\_PUBCOMB.pep:\*

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6: /cgn2\_6/ptodata/2/pubcaa/US07\_PUBCOMB.pep:\*

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9: /cgn2\_6/ptodata/2/pubcaa/US09A\_PUBCOMB.pep:\*

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18: /cgn2\_6/ptodata/2/pubcaa/US10\_NEW\_PUB.PEP:\*

19: /cgn2\_6/ptodata/2/pubcaa/US11A\_PUBCOMB.pep:\*

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21: /cgn2\_6/ptodata/2/pubcaa/US60\_NEW\_PUB.PEP:\*

22: /cgn2\_6/ptodata/2/pubcaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2229	100.0	413	10 US-09-799-978-32	Sequence 32, Appl
2	2229	100.0	413	16 US-10-649-852-32	Sequence 32, Appl
3	1807	81.1	405	10 US-09-799-978-38	Sequence 38, Appl
4	1807	81.1	405	16 US-10-649-852-38	Sequence 38, Appl
5	1804	80.9	411	15 US-10-292-798-636	Sequence 636, Appl
6	1799	80.7	411	9 US-09-881-401-8	Sequence 8, Appl
7	1799	80.7	411	10 US-09-799-978-10	Sequence 10, Appl
8	1799	80.7	411	14 US-10-295-567A-96	Sequence 96, Appl
9	1799	80.7	411	16 US-10-649-852-10	Sequence 10, Appl
10	1799	80.7	411	16 US-10-821-502-8	Sequence 8, Appl
11	1799	80.7	411	16 US-10-757-262-120	Sequence 120, App

Sequence 4, Appl	411	9 US-09-881-401-4	Length 413;
GENERAL INFORMA			
Sequence 18, Appl	411	10 US-09-799-978-18	
Sequence 18, Appl	411	16 US-10-649-852-18	
Sequence 4, Appl	411	16 US-10-821-502-4	
Sequence 14, Appl	397	10 US-09-799-978-4	
Sequence 14, Appl	397	16 US-10-649-852-4	
Sequence 12, Appl	438	10 US-09-799-978-12	
Sequence 12, Appl	438	16 US-10-649-852-12	
Sequence 178, Appl	438	17 US-10-482-029-178	
Sequence 2, Appl	431	9 US-09-881-401-2	
GENERAL INFORMA			
Sequence 2, Appl	431	10 US-09-818-009-13	
Sequence 20, Appl	431	16 US-10-821-502-2	
Sequence 20, Appl	431	16 US-09-799-978-20	
Sequence 10, Appl	431	16 US-10-649-852-20	
Sequence 10, Appl	431	9 US-09-191-724-10	
Sequence 26, Appl	431	10 US-09-818-009-11	
Sequence 26, Appl	431	16 US-10-649-852-26	
Sequence 36, Appl	431	10 US-09-799-978-36	
Sequence 36, Appl	431	15 US-10-649-193-0	
Sequence 129, Appl	431	16 US-10-649-852-24	
Sequence 42, Appl	430	9 US-09-853-386-140	
Sequence 26, Appl	430	10 US-09-799-978-26	
Sequence 26, Appl	430	16 US-10-649-852-26	
Sequence 34, Appl	430	16 US-10-649-852-34	
Sequence 34, Appl	430	16 US-10-649-852-34	
Sequence 2, Appl	420	9 US-09-853-186-129	
Sequence 2, Appl	420	10 US-09-799-978-42	
Sequence 42, Appl	420	10 US-10-649-852-42	
Sequence 42, Appl	420	16 US-10-649-852-34	
Sequence 34, Appl	420	16 US-10-649-852-34	
Sequence 2, Appl	415	9 US-09-191-724-2	
Sequence 2, Appl	415	10 US-09-799-978-2	
Sequence 2, Appl	415	10 US-09-799-978-2	
SEQUENCE 1, Appl	415	14 US-10-242-822B-1	
ORGANISM: Xenopus laevis			
US-09-799-978-32			
Query Match	100.0%	Score 2229;	DB 10;
Best Local Similarity	100.0%	Pred. No. 5.3e-199;	
Matches 413; Conservative	0;	Mismatches 0;	
		Indels 0;	
		Gaps 0;	

RESULT 1

US-09-799-978-32

; Sequence 32, Application US/09799978

; Publication No. US2003016580A1

; GENERAL INFORMATION:

; APPLICANT: The Procter &amp; Gamble Company

; INVENTOR: Isfort, Robert

; APPLICANT: Sheldon, Russell

; TITLE OF INVENTION: Methods for Identifying Compounds for Regulating Muscle Mass or

; TITLE OF INVENTION: Function Using Corticotropin Releasing Factor Receptors

; FILE REFERENCE: 8448

; CURRENT APPLICATION NUMBER: US/09/799,978

; CURRENT FILING DATE: 2001-03-06

; NUMBER OF SEQ ID NOS: 44

; SOFTWARE: Patentin version 3.0

; SEQ ID NO: 32

; LENGTH: 413

; TYPE: PRT

; ORGANISM: Xenopus laevis

US-09-799-978-32

; ALIGNMENTS

; ALIGMENTS

Db 121 INYLGHCISIALVIAFLFLCLRSIRCLRNIIHNLITFLILRNIMWFLQMDHNTI 180

Qy 181 SNEWRCRCTTINYFVVTNFFWMFVEGCYLHTATVMTYSTDKRKWFLFIGCIPSP 240

Db 181 SNEWRCRCTTINYFVVTNFFWMFVEGCYLHTATVMTYSTDKRKWFLFIGCIPSP 240

Qy 241 IWTWAIKLYFENEQCWIGKEPGKTYDYYGRRVILVLLNFVFLNIRLMTKLRAST 300

Db 241 IWTWAIKLYFENEQCWIGKEPGKTYDYYGRRVILVLLNFVFLNIRLMTKLRAST 300

Qy 301 TSETIQRKAVATLVLPLIGITMFLFVNGEDDVSVQFVPSQFQFVSYF 360

Db 301 TSETIQRKAVATLVLPLIGITMFLFVNGEDDVSVQFVPSQFQFVSYF 360

Qy 361 YCFLNGEVRSAARKRWHRWDHSLRVRVARAMS IPTSPTRISFSIKOTAAV 413

Db 361 YCFLNGEVRSAARKRWHRWDHSLRVRVARAMS IPTSPTRISFSIKOTAAV 413

RESULT 2  
US-10-649-852-32  
; Sequence 32, Application US/10649852  
; PUBLICATION NO. US20040101911A1  
; GENERAL INFORMATION:  
; APPLICANT: The Procter & Gamble Company  
; ATTORNEY: Isfort, Robert  
; TITLE OF INVENTION: Methods for Identifying Compounds for Regulating Muscle Mass or Force  
; FILE REFERENCE: 8448R  
; CURRENT APPLICATION NUMBER: US/10/649,852  
; CURRENT FILING DATE: 2003-08-27  
; PRIOR APPLICATION NUMBER: US 09/799,978  
; PRIOR FILING DATE: 2001-03-06  
; NUMBER OF SEQ ID NOS: 44  
; SOFTWARE: Patentin, version 3.0  
; SEQ ID NO: 32  
; LENGTH: 405  
; TYPE: PRT  
; ORGANISM: Xenopus laevis  
; US-10-649-852-32

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Matches 413; Conservative 0; Mismatches 0;

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Db 1 MDSTIPEI1IDBEDANCSLLDAFQDSFLHSESSSPFEGPYCSATIDQIGTCWPRSLAG 60

Qy 61 ELVERCPDSINGIRNTNVRRECFTGWTASMMNYSQCVPLDNRKYYKJALI 120

Db 61 ELVERCPDSINGIRNTNVRRECFTGWTASMMNYSQCVPLDNRKYYKJALI 120

Qy 121 INYLGHCISIALVIAFLFLCLRSIRCLRNIIHNLITFLILRNIMWFLQMDHNTI 180

Db 121 INYLGHCISIALVIAFLFLCLRSIRCLRNIIHNLITFLILRNIMWFLQMDHNTI 180

Qy 181 SNEWRCRCTTINYFVVTNFFWMFVEGCYLHTATVMTYSTDKRKWFLFIGCIPSP 240

Db 181 SNEWRCRCTTINYFVVTNFFWMFVEGCYLHTATVMTYSTDKRKWFLFIGCIPSP 240

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Db 241 IWTWAIKLYFENEQCWIGKEPGKTYDYYGRRVILVLLNFVFLNIRLMTKLRAST 300

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Db 301 TSETIQRKAVATLVLPLIGITMFLFVNGEDDVSVQFVPSQFQFVSYF 360

Qy 361 YCFLNGEVRSAARKRWHRWDHSLRVRVARAMS IPTSPTRISFSIKOTAAV 413

Db 361 YCFLNGEVRSAARKRWHRWDHSLRVRVARAMS IPTSPTRISFSIKOTAAV 413

Db 361 YCFLNGEVRSAARKRWHRWDHSLRVRVARAMS IPTSPTRISFSIKOTAAV 413

RESULT 3  
US-09-799-978-38  
; Sequence 38, Application US/09799978  
; PUBLICATION NO. US20030165807A1  
; GENERAL INFORMATION:  
; APPLICANT: The Procter & Gamble Company  
; ATTORNEY: Isfort, Robert  
; TITLE OF INVENTION: Methods for Identifying Compounds for Regulating Muscle Mass or Force  
; FILE REFERENCE: 8448  
; CURRENT APPLICATION NUMBER: US/09/799,978  
; CURRENT FILING DATE: 2001-03-06  
; NUMBER OF SEQ ID NOS: 44  
; SOFTWARE: Patentin, version 3.0  
; SEQ ID NO: 38  
; LENGTH: 405  
; TYPE: PRT  
; ORGANISM: Ameiurus nebulosus  
; US-09-799-978-38

Query Match 81.1%; Score 1807; DB 10; Length 405;  
Best Local Similarity 79.9%; Pred. No. 1.e-159; Mismatches 42; Indels 8; Gaps 2;  
Matches 330; Conservative 33; Mismatches 42; Indels 8; Gaps 2;

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Db 53 RVVARCPDPFINGTCKNNSRATRECLENGTWAKFINTSCEPFLERGRKYPYKJALI 112

Qy 121 INYLGHCISIALVIAFLFLCLRSIRCLRNIIHNLITFLILRNIMWFLQMDHNTI 180

Db 113 INYLGHCISVGRVAVFLCLRSIRCLRNIIHNLITFLILRNIMWFLQMDHNTI 172

Qy 181 SNEYWCRCTTINYFVVTNFFWMFVEGCYLHTATVMTYSTDKRKWFLFIGCIPSP 240

Db 173 RNEPACRLLTIVNFVVTNFFWMFVEGCYLHTATVMTYSTDKRKWFLFIGCIPCPV 232

Qy 241 IWTWAIKLYFENEQCWIGKEPGKTYDYYGRRVILVLLNFVFLNIRLMTKLRAST 300

Db 233 IIAVAGKLYNEOCWFKERPEGRKYYDYYGPFVTVLNFVFLNIRLMTKLRAST 292

Qy 301 TSETIQRKAVATLVLPLIGITMFLFVNGEDDVSVQFVPSQFQFVSYF 360

Db 293 TSETIQRKAVATLVLPLIGITMFLFVNGEDDVSVQFQFVSYF 352

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RESULT 4  
US-10-649-852-38  
; Sequence 38, Application US/10649852  
; PUBLICATION NO. US20040101911A1  
; GENERAL INFORMATION:  
; APPLICANT: The Procter & Gamble Company  
; ATTORNEY: Isfort, Robert  
; TITLE OF INVENTION: Methods for Identifying Compounds for Regulating Muscle Mass or Force  
; FILE REFERENCE: 8448R  
; CURRENT APPLICATION NUMBER: US/10/649,852  
; CURRENT FILING DATE: 2003-08-27  
; PRIOR APPLICATION NUMBER: US 09/799,978  
; PRIOR FILING DATE: 2001-03-06  
; NUMBER OF SEQ ID NOS: 44

SOFTWARE: PatentIn version 3.0  
 SEQ ID NO 38  
 LENGTH: 405  
 TYPE: PRT  
 ORGANISM: Ameiurus nebulosus  
 US-10-649-852-38

Query Match 81.1%; Score 1807; DB 16; Length 405;  
 Best Local Similarity 79.9%; Pred. No. 1..1e-159;  
 Matches 330; Conservative 33; Mismatches 42; Indels 8; Gaps 2;  
 Query 1 MDSTIFETIIDEFDANCSLLDAFQDSPLHSSSSSSPFGPYCSATIDQIGTCWPRSLAG 60  
 Db 1 MEVSLLEL--SVEVNCSLADAFGDPAGNDSL---YCNAATADEIGTCWPRSGAG 52  
 Query 61 ELVERPCPDSENGFIRNTNTNRYRECENGFTASWNY SQCVLPIDNKRKYALHYKALI 120  
 Db 53 RUVVARPCCPDFINGVKYNSTRSARECTENGTFWAKINNSCEPILEBKRYPVHYKALI 112  
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 Db 13 INYLGHCISVGLALVIAFLFLCLRSIRCLRNTHWNLITTLRNTRNMFQIMDENEHE 172  
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 Db 173 RNEPWCRLITTYNPFVTFNFFWVYEGCYLHTAIVMTYSTDKLRKWVFLPTGWCIPCPV 232  
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 Db 233 TIAWAVGKLYNEEQCMQIGKEPGKYDYYQCRVILVLYNIVLNFVNTRNMFQIMDENEHE 292  
 Query 301 TSETIQRKAVATLVLPLGLITMFLFVNGEDDDYSQIVYIYNSFLQSFGQFVVSVF 360  
 Db 293 TSETIQRKAVATLVLPLGLITMFLFVNGEDDDYSQIVYIYNSFLQSFGQFVVSVF 352  
 Query 361 YCFLNGEVYRSAARKRMRWQDHSLRVYVARAMSIPSPTRSFHSIKQTAVY 413  
 Db 353 YCFLNGEVYRSAARKRMRWQDHSLRVYVARAMSIPSPTRSFHSIKQTAVY 405

RESULT 6  
 US-10-292-798-636  
 / Sequence 636, Application US/10292798  
 / Publication No. US2010303583341  
 / GENERAL INFORMATION  
 / APPLICANT: SUWA, MAKIKO  
 / APPLICANT: ASAI, KIYOSHI  
 / APPLICANT: AKIYAMA, YUTOSHI  
 / APPLICANT: ABURATANI, HIROTUKI  
 / TITLE OF INVENTION: GUANOSINE TRIPHOSPHATE-BINDING PROTEIN COUPLED RECEPTORS  
 / FILE NUMBER: 08/325,166  
 / CURRENT APPLICATION NUMBER: US/10/292,798  
 / CURRENT FILING DATE: 2002-11-13  
 / PRIOR APPLICATION NUMBER: 10/017,161  
 / PRIOR FILING DATE: 2001-12-18  
 / PRIOR APPLICATION NUMBER: JP 2001-246789  
 / PRIOR FILING DATE: 2001-06-18  
 / NUMBER OF SEQ ID NOS: 2070  
 / SOFTWARE: PatentIn Ver. 2.1  
 / SEQ ID NO 636  
 / LENGTH: 411  
 / TYPE: PRT  
 / ORGANISM: Homo sapiens  
 US-10-292-798-636

Query Match 80.9%; Score 1804; DB 15; Length 411;  
 Best Local Similarity 80.0%; Pred. No. 2..1e-155;  
 Matches 333; Conservative 33; Mismatches 42; Indels 8; Gaps 4;  
 Query 1 MDSTIFETIIDEFDANCSLLDAFQDSPLHSSSSSSPFGPYCSATIDQIGTCWPRSL 58  
 Db 1 MDAAHLHSLL--EANCSL--ALAEELLDGWPPLDBPGPYSYCNLTDQIGTCWPRSA 55

Qy 59 AGEYVERPCPDSENGFIRNTNTNRYRECENGFTASWNY SQCVLPIDNKRKYALHYK 117  
 Db 56 AGALYVERPCBEYFNVKNTTRNAYRECLNGFTASWNY SQCVLPIDNKRKYALHYK 115  
 Qy 118 ALIINYLGHCRISILALVIAFLFLCLRSIRCLRNTHWNLITTLRNTRNMFQIMDHN 177  
 Db 116 ALVNVYLGHCVSVAALVAAFLFLARSIRCLRNTHWNLITTLRNTRNMFQIMDHN 175  
 Qy 178 IHESENEWWCRCITIINYFVTFNFFWVYEGCYLHTAIVMTYSTDKLRKWVFLPTGWCIP 237  
 Db 176 VHESENEWWCRCITIINYFVTFNFFWVYEGCYLHTAIVMTYSTDKLRKWVFLPTGWCIP 235  
 Qy 238 SPLITVWAICKLFLYNEQCMQIGKEPGKYDYYQCRVILVLYNIVLNFVNTRNMFQIMDENEHE 297  
 Db 236 SPLITVWAICKLFLYNEQCMQIGKEPGKYDYYQCRVILVLYNIVLNFVNTRNMFQIMDENEHE 295  
 Qy 298 ASTTSETIQRKAVATLVLPLGLITMFLFVNGEDDDYSQIVYIYNSFLQSFGQFVVSVF 357  
 Db 296 ASTTSETIQRKAVATLVLPLGLITMFLFVNGEDDDYSQIVYIYNSFLQSFGQFVVSVF 355  
 Qy 358 SVFYCFLNGEVYRSAARKRMRWQDHSLRVYVARAMSIPSPTRSFHSIKQTAVY 413  
 Db 356 SVFYCFLNGEVYRSAARKRMRWQDHSLRVYPMARAMSIPSPTRSFHSIKQTAVY 411

NUMBER OF SEQUENCES: 8  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Seed Intellectual Property Law Group  
 STREET: 701 Fifth Avenue, Suite 6300  
 CITY: Seattle  
 STATE: Washington  
 COUNTY: USA  
 ZIP: 98104-7092  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/881,401  
 FILING DATE: 13-Jun-2001  
 CLASSIFICATION: <Unknown>  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Christensen, William T.  
 REGISTRATION NUMBER: 44,514  
 REFERENCE/DOCKET NUMBER: 690068-401C4  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (206) 622-4900  
 TELEFAX: (206) 682-6031  
 INFORMATION FOR SEQ ID NO: 8:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 411 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 SEQUENCE DESCRIPTION: SEQ ID NO: 8:  
 US-09-881-401-8

Query Match 80.7%; Score 1799; DB 9;  
 Best Local Similarity 79.8%; Pred. No. 6..2e-159;  
 Db

Matches 332; Conservative 33; Mismatches 43; Indels 8; Gaps 4; Db 236 FPIIVAWAIGKLYENQCWGKEPGLDLYD1YQGPILVLLINFPVTRILMTKL 295

Qy 1 MDSTFELIIDDEFDANCSSLDAQDSFLRSESSSPFGFSGP--YCSATIDQIGTCWPSL 58

Db 1 MDAALHSLI--EANCSL--ALAEFLIDLGWGPPLDPGPYSCTNTIDQIGTCWPSA 55

Qy 59 AGELVERCPDPSFNGTRYNTRVRECENGTWASWMDNSQCPVILDK-RKVALHYKI 117

Db 56 AGALVERCPDPSFNGTRYNTRVRECENGTWASKINYQCPVILDKQKRDLYHRI 115

Qy 118 ALIINYLGHCISILALVIAFLFLCIRSIRCLRNTHWNLLITFLRNWFLQIMIDHN 177

Db 116 ALVNVLGHCVSVAALVAFLLFLAARSIRCLRNTHWNLLITFLRNWFLQIMDHE 175

RESULT 8  
US-10-225-567A-96

Qy 178 THESEWVRCITIINYKVTINFFWMFEGCILTAITMTYSDKLKRWVFLIGQTP 237

Db 176 VHESEWVHCITIINYKVTINFFWMFEGCILTAITMTYSTERLRLCFLFIGWCIP 235

Qy 238 SPIIVTWAICKLFYNEQWCMIGKEPKGYDYYQGRVILVLLINFPFLNIVRILMTKL 297

Db 236 SPIIVTWAICKLFYNEQWCMIGKEPKGYDYYQGRVILVLLINFPFLNIVRILMTKL 295

Qy 298 ASTTSETIYQRKAVATLFLPLIGTYMFVNGEDDVSQVTFYNSFLOSFGFEPY 357

Db 296 ASTTSETIYQRKAVATLFLPLIGTYMFVNGEDDVSQMFYNSFLOSFGFEPY 355

Qy 358 SVFVCFLEGEVRSARKRWRQDHSLSRVARAMSITSPTRISPSIKOTAAV 413

Db 356 SVFVCFLEGEVRSARKRWRQDHSLSRVPMARAMSITSPTRISPSIKOTAAV 411

RESULT 9  
US-10-225-567A-96

Qy 178 THESEWVRCITIINYKVTINFFWMFEGCILTAITMTYSDKLKRWVFLIGQTP 237

Db 176 VHESEWVHCITIINYKVTINFFWMFEGCILTAITMTYSTERLRLCFLFIGWCIP 235

Qy 238 SPIIVTWAICKLFYNEQWCMIGKEPKGYDYYQGRVILVLLINFPFLNIVRILMTKL 297

Db 236 SPIIVTWAICKLFYNEQWCMIGKEPKGYDYYQGRVILVLLINFPFLNIVRILMTKL 295

Qy 298 ASTTSETIYQRKAVATLFLPLIGTYMFVNGEDDVSQVTFYNSFLOSFGFEPY 357

Db 296 ASTTSETIYQRKAVATLFLPLIGTYMFVNGEDDVSQMFYNSFLOSFGFEPY 355

Qy 358 SVFVCFLEGEVRSARKRWRQDHSLSRVARAMSITSPTRISPSIKOTAAV 413

Db 356 SVFVCFLEGEVRSARKRWRQDHSLSRVPMARAMSITSPTRISPSIKOTAAV 411

RESULT 10  
US-10-649-852-10

Qy 178 THESEWVRCITIINYKVTINFFWMFEGCILTAITMTYSDKLKRWVFLIGQTP 237

Db 176 VHESEWVHCITIINYKVTINFFWMFEGCILTAITMTYSTERLRLCFLFIGWCIP 235

Qy 238 SPIIVTWAICKLFYNEQWCMIGKEPKGYDYYQGRVILVLLINFPFLNIVRILMTKL 297

Db 236 SPIIVTWAICKLFYNEQWCMIGKEPKGYDYYQGRVILVLLINFPFLNIVRILMTKL 295

Qy 298 ASTTSETIYQRKAVATLFLPLIGTYMFVNGEDDVSQVTFYNSFLOSFGFEPY 357

Db 296 ASTTSETIYQRKAVATLFLPLIGTYMFVNGEDDVSQMFYNSFLOSFGFEPY 355

Qy 358 SVFVCFLEGEVRSARKRWRQDHSLSRVARAMSITSPTRISPSIKOTAAV 413

Db 356 SVFVCFLEGEVRSARKRWRQDHSLSRVPMARAMSITSPTRISPSIKOTAAV 411

GENERAL INFORMATION:

ORGANISM: Homo sapiens

SEQUENCE 96; Application US/10225567A

Publication No. US20030113798A1

GENERAL INFORMATION:

APPLICANT: Lifespan Biosciences

Brown, Joseph P.

Burmer, Glema C.

APPLICANT: Rough, Christine L.

APPLICANT: TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS

FILE REFERENCE: 1920-4-4

CURRENT APPLICATION NUMBER: US/10/225, 567A

CURRENT FILING DATE: 2001-12-19

PRIOR APPLICATION NUMBER: 60/257, 144

PRIOR FILING DATE: 2000-12-19

NUMBER OF SEQ ID NOS: 292

SOFTWARE: PatentIn version 3.1

SEQ ID NO 96

LENGTH: 411

TYPE: PRT

ORGANISM: Homo sapiens

US-10-225-567A-96

Query Match 80.7%; Score 1799; DB 14; Pred. No. 6.2e-159; Best Local Similarity 79.8%; Mismatches 33; Indels 8; Gaps 4; Matches 332; Conservative 33; Software: PatentIn version 3.1

Qy 1 MDSTFELIIDDEFDANCSSLDAQDSFLRSESSSPFGFEPY - YCSATIDQIGTCWPSL 58

Db 1 MDAALHSLI--EANCSL--ALAEFLIDLGWGPPLDPGPYSCTNTIDQIGTCWPSA 55

Qy 59 AGELVERCPDPSFNGTRYNTRVRECENGTWASWMDNSQCPVILDK-RKVALHYKI 117

Db 56 AGALVERCPDPSFNGTRYNTRVRECENGTWASKINYQCPVILDKQKRDLYHRI 115

Qy 118 ALIINYLGHCISILALVIAFLFLCIRSIRCLRNTHWNLLITFLRNWFLQIMIDHN 177

Db 116 ALVNVLGHCVSVAALVAFLLFLAARSIRCLRNTHWNLLITFLRNWFLQIMDHE 175

Qy 178 IHESNEWRCITIINYKVTINFFWMFEGCILTAITMTYSDKLKRWVFLIGQTP 237

Db 176 VHESEWVHCITIINYKVTINFFWMFEGCILTAITMTYSTERLRLCFLFIGWCIP 235

Qy 238 SPIIVTWAICKLFYNEQWCMIGKEPKGYDYYQGRVILVLLINFPFLNIVRILMTKL 297

Db 236 SPIIVTWAICKLFYNEQWCMIGKEPKGYDYYQGRVILVLLINFPFLNIVRILMTKL 295

Qy 298 ASTTSETIYQRKAVATLFLPLIGTYMFVNGEDDVSQVTFYNSFLOSFGFEPY 357

Db 296 ASTTSETIYQRKAVATLFLPLIGTYMFVNGEDDVSQMFYNSFLOSFGFEPY 355

Qy 358 SVFVCFLEGEVRSARKRWRQDHSLSRVARAMSITSPTRISPSIKOTAAV 413

Db 356 SVFVCFLEGEVRSARKRWRQDHSLSRVPMARAMSITSPTRISPSIKOTAAV 411

GENERAL INFORMATION:

APPLICANT: The Procter & Gamble Company  
 APPLICANT: Isfort, Robert  
 APPLICANT: Sheldon, Russell  
 TITLE OF INVENTION: Methods for Identifying Compounds for Regulating Muscle Mass or Force  
 FILE REFERENCE: 8448R  
 CURRENT APPLICATION NUMBER: US/10/649, 852  
 CURRENT FILING DATE: 2003-08-27  
 PRIOR APPLICATION NUMBER: US 09/799,978  
 PRIOR FILING DATE: 2001-03-06  
 NUMBER OF SEQ ID NOS: 44  
 SOFTWARE: PatentIn version 3.0  
 SEQ ID NO 10  
 LENGTH: 411  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-10-649-852-10

Query Match 80.7%; Score 1799; DB 16; Length 411;  
 Best Local Similarity 79.8%; Pred. No. 6.2e-159;  
 Matches 332; Conservative 33; Mismatches 43; Indels 8; Gaps 4;  
 US-10-821-502-8

Qy 1 MDSTIFFIIDEFDANSCLDAFQDSFHSESSSSFFRGFP -YCSATIDQIGTCMPSRL 58  
 Db 1 MDAAHLHSL--EANCSL- ALAEEULLDGGPLDPGEGPSYCNTLDDQIGTCMPSA 55

Qy 59 AGELVERPCPDSPFGNTTRYNTTRVYRECENGTWASMMYNSQCVPLDNK-RKVAlHYKI 117  
 Db 56 AGALVERPCPEFGVKNTTENAYRECLENGTWASMMYNSQCVPLDNK-RKVAlHYKI 115

Qy 118 ALINTVGHGICISLALVAVFLPLCLASIRCERNLHWNLTTFIRNMMFLQDIDHN 177  
 Db 116 ALVNVYLGHCVSAALVAVFLPLFLASIRCERNVTHWNLTTFIRNMMFLQDIDHN 175

Qy 178 THESNNEWCRCTTINYFVNTNFNMFVEGCTLHTAVMTYSTDKLRKAYFLFIGWCIP 237  
 Db 176 VHSNEWVHCCTTINYFVNTNFNMFVEGCTLHTAVMTYSTDKLRKAYFLFIGWCIP 235

Qy 238 SPTIVTWACKFLFENBQCGWIGKTYDLYQGRVLYLILNFELVNLTVRLMTKL R 297  
 Db 236 FPIIVAWVIGKLYTENECWFGEKGPDGIVDVTYQGPFLVLLNFVFLNTRMLKL R 295

Qy 258 ASTTSETTQYRKAVKATVYLPLGLITMMLPFVNGDVSQIVYFNSPLQSPQGFV 357  
 Db 256 ASTTSETTQYRKAVKATVYLPLGLITMMLPFVNGDLSQMFYFNSPLQSPQGFV 355

Qy 358 SVFYCFNNGEVRSAAKWRHWRQDHHSIRVRYARAMSPTSPTRISPHSIKOTAAV 413  
 Db 356 SVFYCFNNGEVRSAAKWRHWRQDHHSIRVPMARMSPTSPTRISPHSIKOTAAV 411

RESULT 10  
 US-10-821-502-8  
 ; Sequence 8, Application US/10821502  
 ; Publication No. US20040105533A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Lovenberg, Timothy W.  
 ; Oliersdorf, Tilmann  
 ; Liaw, Chen Wang  
 ; Grigoriadis, Dimitri E.  
 ; Chalmers, Derek T.  
 ; DeSouza, Erol B.  
 ; TITLE OF INVENTION: CORTICOTROPIN RELEASING FACTOR 2  
 ; NUMBER OF SEQUENCES: 8  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSE: Seed Intellectual Property Law Group  
 ; STREET: 701 Fifth Avenue, Suite 6300  
 ; CITY: Seattle  
 ; STATE: Washington  
 ; COUNTRY: USA  
 ; ZIP: 98104-7092  
 ; COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/10/821-502  
 FILING DATE: 09-Apr-2004  
 CLASSIFICATION: <Unknown>  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Christiansen, William T.  
 REGISTRATION NUMBER: 14,14  
 REFERENCE/DOCKET NUMBER: 690068-40105  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (206) 522-4900  
 TELEFAX: (206) 682-6031  
 INFORMATION FOR SEQ ID NO: 8:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 411 amino acids  
 TYPE: amino acid  
 TOPOLOGY: Linear  
 MOLECULE TYPE: protein  
 SEQUENCE DESCRIPTION: SEQ ID NO: 8:  
 US-10-821-502-8

Query Match 80.7%; Score 1799; DB 16; Length 411;  
 Best Local Similarity 79.8%; Pred. No. 6.2e-159;  
 Matches 332; Conservative 33; Mismatches 43; Indels 8; Gaps 4;  
 US-10-821-502-8

Qy 1 MDSTIFFIIDEFDANSCLDAFQDSFHSESSSSFFRGFP -YCSATIDQIGTCMPSRL 58  
 Db 1 MDAAHLHSL--EANCSL- ALAEEULLDGGPLDPGEGPSYCNTLDDQIGTCMPSA 55

Qy 59 AGELVERPCPDSPFGNTTRYNTTRVYRECENGTWASMMYNSQCVPLDNK-RKVAlHYKI 117  
 Db 56 AGALVERPCPEFGVKNTTENAYRECLENGTWASMMYNSQCVPLDNK-RKVAlHYKI 115

Qy 118 ALINTVGHGICISLALVAVFLPLCLASIRCERNLHWNLTTFIRNMMFLQDIDHN 177  
 Db 116 ALVNVYLGHCVSAALVAVFLPLFLASIRCERNVTHWNLTTFIRNMMFLQDIDHN 175

Qy 178 THESNNEWCRCTTINYFVNTNFNMFVEGCTLHTAVMTYSTDKLRKAYFLFIGWCIP 237  
 Db 176 VHSNEWVHCCTTINYFVNTNFNMFVEGCTLHTAVMTYSTDKLRKAYFLFIGWCIP 235

Qy 238 SPTIVTWACKFLFENBQCGWIGKTYDLYQGRVLYLILNFELVNLTVRLMTKL R 297  
 Db 236 FPIIVAWVIGKLYTENECWFGEKGPDGIVDVTYQGPFLVLLNFVFLNTRMLKL R 295

Qy 258 ASTTSETTQYRKAVKATVYLPLGLITMMLPFVNGDVSQIVYFNSPLQSPQGFV 357  
 Db 256 ASTTSETTQYRKAVKATVYLPLGLITMMLPFVNGDLSQMFYFNSPLQSPQGFV 355

Qy 358 SVFYCFNNGEVRSAAKWRHWRQDHHSIRVRYARAMSPTSPTRISPHSIKOTAAV 413  
 Db 356 SVFYCFNNGEVRSAAKWRHWRQDHHSIRVPMARMSPTSPTRISPHSIKOTAAV 411

RESULT 11  
 US-10-757-262-120  
 ; Sequence 120, Application US/10757262  
 ; Publication No. US2004197325A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Karicheti, Venkateswarlu  
 ; APPLICANT: Silos-Santiago, Inmaculada  
 ; APPLICANT: Eliasof, Scott D.  
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING  
 ; UROLOGICAL DISORDERS USING 44390, 54181, 211, 5687, 884,  
 ; 1405, 636, 4421, 5410, 30005, 16405, 18560, 2047,  
 ; 33751, 52872, 14063, 20739, 32244, 43239, 44333, 51164,  
 ; 53010, 16852, 1587, 2207, 22245, 2387, 52908, 69112, 14900,  
 ; 18547, 115, 579, 1595, 15625, 760, 18603, 2354, 34620, 577, 619, 1423,  
 ; 32720, 4809, 14403, 16816, 1787, 1656, 2354, 34620, 577, 619, 1423,  
 ; 2158, 8263, 15402, 16209, 16385, 21165, 30911, 41897, 1643,

TITLE OF INVENTION: 2543, 9626, 13231, 32409, 84260, 2882, 8203, 32678 OR  
 TITLE OF INVENTION: 55053  
 FILE REFERENCE: MP03-00071R0NM  
 CURRENT APPLICATION NUMBER: US10/757,262  
 CURRENT FILING DATE: 2004-01-14  
 PRIOR APPLICATION NUMBER: US 60/440,318  
 PRIOR FILING DATE: 2003-01-15  
 PRIOR APPLICATION NUMBER: US 60/444,783  
 PRIOR FILING DATE: 2003-02-04  
 PRIOR APPLICATION NUMBER: US 60/457,901  
 PRIOR FILING DATE: 2003-03-27  
 PRIOR APPLICATION NUMBER: US 60/468,775  
 PRIOR FILING DATE: 2003-05-08  
 PRIOR APPLICATION NUMBER: US 60/471,614  
 PRIOR FILING DATE: 2003-05-19  
 PRIOR APPLICATION NUMBER: US 60/478,742  
 PRIOR FILING DATE: 2003-06-16  
 PRIOR APPLICATION NUMBER: US 60/488,529  
 PRIOR FILING DATE: 2003-07-18  
 PRIOR APPLICATION NUMBER: US 60/491,156  
 PRIOR FILING DATE: 2003-07-30  
 PRIOR APPLICATION NUMBER: US 60/499,594  
 PRIOR FILING DATE: 2003-09-02  
 PRIOR APPLICATION NUMBER: US 60/506,332  
 PRIOR FILING DATE: 2003-09-26  
 NUMBER OF SEQ ID NOS: 136  
 SOFTWARE: FASTSEQ FOR Windows Version 4.0  
 SEQ ID NO: 120  
 LENGTH: 411  
 TYPE: PRY  
 ORGANISM: Homo sapiens  
 US-10-757-262-120

Query Match 80.7%; Score 1799; DB 16; Length 411;

Best Local Similarity 79.8%; Pred. No. 6.2e-159; Mismatches 33; Indels 8; Gaps 4;

US-10-757-262-120

Query 1 MDSTFEIILIDFEDANCSLLDAFQDSFLHSESSSSFFGFRGP--YCSATIDQIGTCWPRSL 58  
 Db 1 MDAALHSLL--EANCSL--ALABELLQWGPPLDPPEPYSCTTIDQIGTCWPRSA 55  
 Query 59 AGELYVERPCPDSENGTRYNTTRVYRECFENGTWASWMNYSQCYPBILDNK-RKYALHYKI 117  
 Db 56 AGALYVERPCPEYNGKYNTTRNAYRECLENGTWASKINYSQCYPBILDKQRKYDLHYKI 115  
 Query 118 ALIINYLGHCISILALVIAFLCLRSFLCLRNITIHWNLITTFILRNWFLQMTDEN 177  
 Db 116 ALIINYLGHCYSVVAFLVAFLFLAFLSFLCLRNITIHWNLITTFILRNWFLQQLDIE 175  
 Query 178 IHESNWVRCCITIILYNYFVTFNFFWMFVEGCYLHTATIYMTSTDKLKRWVFLFGWCIP 237  
 Db 176 VHESNWVRCHCITIIFNYFVTFNFFWMFVEGCYLHTATIYMTSTDKLKRWVFLFGWCIP 235  
 Query 238 SPLITVWAIICKLFYENEQCNGKIGPKYIDYIYQGRVILVILLNFVFLNIVRLMTKLR 297  
 Db 236 EPILVAWAIGKLYENEQCNGKIGPKYIDYIYQGRVILVILLNFVFLNIVRLMTKLR 295  
 Query 358 SVFYCPFLNGEVRSAARKRWHRQDHSLRVRVARAMSIPTSPTRISFSIKQTAAV 413  
 Db 356 SVFYCPFLNGEVRSAARKRWHRQDHSLRVRVARAMSIPTSPTRISFSIKQTAAV 411  
 RESULT 12  
 US-09-881-401-4  
 Sequence 4, Application US/09881401  
 Patent No. US20020077458A1  
 GENERAL INFORMATION:  
 APPLICANT: Lovenberg, Timothy W.  
 Oltersdorff, Timman

Query 125 ASTSETIYQRKAVATLVLPLIGITMUFFVNGEDVSQIYIYFNSFLQSFGFVY 357  
 Db 126 ASTSETIYQRKAVATLVLPLIGITMUFFVNGEDVSQIYIYFNSFLQSFGFVY 355  
 Query 358 SVFYCPFLNGEVRSAARKRWHRQDHSLRVRVARAMSIPTSPTRISFSIKQTAAV 413  
 Db 356 SVFYCPFLNGEVRSAARKRWHRQDHSLRVRVARAMSIPTSPTRISFSIKQTAAV 411  
 RESULT 13

US-09-818-009-12

GENERAL INFORMATION:

APPLICANT: THE SALK INSTITUTE FOR BIOLOGICAL STUDIES

TITLE OF INVENTION: UROCORTIN PEPTIDES

NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESS:

ADDRESSEE: FITCH, EVEN, TABIN & FLANNERY

STREET: 120 S. LaSalle Street, Suite 1600

CITY: Chicago

STATE: Illinois

COUNTRY: USA

ZIP: 60603

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/818,009

FILING DATE: 26-Mar-2001

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/981,189

FILING DATE: 10-DEC-1997

APPLICATION NUMBER: US 60/028,144

FILING DATE: 13-JUN-1995

APPLICATION NUMBER: US 60/002,223

FILING DATE: 11-AUG-1995

ATTORNEY/AGENT INFORMATION:

NAME: Schumann, James J.

REGISTRATION NUMBER: 20,856

REFERENCE/DOCKET NUMBER: 57611

TELECOMMUNICATION INFORMATION:

TELEPHONE: 858-552-1311

TELEFAX: 858-552-0095

SEQUENCE DESCRIPTION: SEQ ID NO: 12:

us-09-818-009-12

Query Match 80.4%; Score 1793; DB 10; Length 411;

Best Local Similarity 80.0%; Pred. No. 2, 3e-158; Mismatches 45; Indels 8; Gaps 4;

Matches 333; Conservative 30; MisMatches 45; Indels 8; Gaps 4;

Qy 1 MDSTIPEIIIDFADNSLLDAFQDPLHSESSSSFFGPEGP--YCSATIDQIGTCMPSRL 58

Db 1 MDAA--LILSLIANCESL--ALAEELLDGGMGEPDPDEGYSYCNLTDQIGTCMPSQA 55

Qy 59 AGELVERPCPDSENGIRNTTRVYRECENGTFWASWMSYSCQVPLDNLK-RKYALHYKI 117

Db 56 PGALVERPCPDSENGIRNTTRVYRECENGTFWASWMSYSCQVPLDNLK-RKYALHYKI 115

Qy 118 ALITINYLGHCISIYLALVIAFLFLCLRSIRCLRNIIHWNLITTFILRNIMFLLQIDHN 177

Db 116 ALITINYLGHCISIYLALVIAFLFLCLRSIRCLRNIIHWNLITTFILRNIMFLLQIDHE 175

Qy 178 IHESENNEWCRCTTINYFVTFNFTMFVFGCYLHTAIVMTYSTDKLRKWLFLFGWCIP 237

Db 176 VHEGNEWCRCVTTLFNFVTFNFTMFVFGCYLHTAIVMTYSTDKLRKWLFLFGWCIP 235

Qy 238 SPIVTTWAICKLTFYNEQWIGKEPKGKTDYIYQGRVLVILINFVPLNITRILATKLR 297

Db 236 CPIVAWAVGLEYNEQCWFGKEPDLDVYIYQGPFLVILINFVPLNITRILATKLR 295

Qy 298 ASTTSETIQTYRKAVATVLLPLGIGTYMLFFVNPQGDDYPSQIVTFYFNSPLQSFGFFV 357

Db 296 ASTTSETIQTYRKAVATVLLPLGIGTYMLFFVNPQGDDYPSQIVTFYFNSPLQSFGFFV 355

Qy 358 SVFVCFNGEYRSARKRWHRWDHHSLSRVARAMSPTSPTRISFSHSIKOTAAV 413

Db 356 SVFVCFNGEYRSARKRWHRWDHHSLSRVARAMSPTSPTRISFSHSIKOTAAV 411

RESULT 15

US-10-649-852-18

Sequence 18, Application US/10649852

Publication No. US20040101911A1

GENERAL INFORMATION:

APPLICANT: Isfort, Robert

APPLICANT: Sheldon, Russell

TITLE OF INVENTION: Methods for Identifying Compounds for Regulating Muscle Mass or

TITLE OF INVENTION: Using Corticotropin Releasing Factor Receptors

FILE REFERENCE: 8448R

CURRENT APPLICATION NUMBER: US/10/649,852

CURRENT FILING DATE: 2003-08-27

PRIOR APPLICATION NUMBER: US 09/799,978

PRIOR FILING DATE: 2001-03-06

NUMBER OF SEQ ID NOS: 44

SEQUENCE DESCRIPTION: Patent in version 3.0

SEQ ID NO: 18

LENGTH: 411

TYPE: PRT

ORGANISM: Rattus norvegicus

US-10-649-852-18

RESULT 14

US-09-799-978-18

Sequence 18, Application US/09799978

```

Query Match      80.4%;  Score 1793;  DB 16;  Length 411;
Best Local Similarity 80.0%;  Pred. No. 2.3e-158;
Matches 333;  Conservative 30;  Mismatches 45;  Indels 8;  Gaps 4;
Matches 333;  Conservatve 30;  Mismatches 45;  Indels 8;  Gaps 4;

Qy      1 MDSTIFBIIIDEFDANCSLIDAQDPSFLHSBSSSPGFEGP--YCSATLDQ1GTCWPQSL 58
Db      1 MDAA--LLSLLEANCSL--ALABELLLDGWGBPDPGSPYSICNTLDQ1GTCWPQSA 55

Qy      59 AGELYVERPCPDSENGRYNTTRNYYRECPENGTWASWNNYSCQVPLDNNK-RCYALHYK 117
Db      56 PGALVERPCPBYFNGKYNTTRNAYRECLENGTWASRINSHCBEPLDQQRKDLYTRI 115

Qy      118 ALIINYIGHCISILALVIAPIPLCILRSRCLRNTHNNLITTEFLRNIMWELLQMDHN 177
Db      116 ALIINYLGHCVSVAVALVAAPIPLFLVLRSTRCLRNTHNNLITTEFLRNITWFLQLIDIE 175

Qy      178 IHESENEWWCRCCITTYNFFVVTNFVWMMFEGCYLHTAITMTYSDDKLRKWVFLPIGWCP 237
Db      176 VHEGNEWWCRCCVTTIFNYFVVTNFVWMMFEGCYLHTAITMTYSPFHLRMWFLPIGWCP 235

Qy      238 SPIIYTWAICKLFYENEQCMWCKEPEKYIDTYOGRVIVLILNFVFLNIVRILMTKLR 297
Db      236 CPIIYAWAVGKLYENEQCMWGFKEPGDLDWXYIQQPIIPLVLLINFLNIVRILMTKLR 295

Qy      298 ASTTSEBTIOYRKAVAKATLVLPLGLITYMUFFVNPGEDDVSQIVFYHNSFLOSFOGFYV 357
Db      296 ASTTSEBTIOYRKAVAKATLVLPLGLITYMUFFVNPGEDDVSQIVFYHNSFLOSFOGFYV 355

Qy      358 SVFYCFLNGEVRSAAKRKRWRWODHSLRVARAMSISPTSPTRSPSIKOTAV 413
Db      356 SVFYCFFNGEVRSALRKKRWRWODHSLRVARAMSISPTSPTRSPSIKOTAV 411

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Search completed: August 20, 2005, 00:42:16  
 Job time : 165 sec

GenCore version 5.1.6  
Copyright (C) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using SW model

Run on: August 20, 2005, 00:23:03 ; Search time 43 Seconds  
(without alignments)  
716.978 Million cell updates/sec

Title: US-10-649-852-32  
Perfect score: 2229  
Sequence: 1 MDSTIPEIIDEPDANCSSL.....SIPTSPTRISFSIKQTAAV 413

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing First 45 summaries

Database : Issued Patents AA:  
1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep:  
2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep:  
3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep:  
4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep:  
5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep:  
6: /cgn2\_6/ptodata/1/iaa/backfile1.pep:  
\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	2229	100.0	413	4	US-09-799-978-32	Sequence 32, App1
2	1807	81.1	405	4	US-09-799-978-38	Sequence 38, App1
3	1804	80.9	411	4	US-09-631-603-12	Sequence 12, App1
4	1799	80.7	411	4	US-08-381-433A-8	Sequence 8, App1
5	1799	80.7	411	4	US-09-799-978-10	Sequence 10, App1
6	1799	80.7	411	4	US-09-88-401-8	Sequence 9, App1
7	1793	80.4	411	3	US-08-381-433A-4	Sequence 4, App1
8	1793	80.4	411	3	US-08-981-1895-12	Sequence 12, App1
9	1793	80.4	411	4	US-09-799-978-18	Sequence 18, App1
10	1793	80.4	411	4	US-09-881-401-4	Sequence 4, App1
11	1787.5	80.2	397	4	US-09-799-978-14	Sequence 14, App1
12	1786	80.1	438	4	US-09-799-978-12	Sequence 12, App1
13	1784.5	80.1	431	3	US-08-1893-13	Sequence 13, App1
14	1784.5	80.1	431	4	US-09-881-401-2	Sequence 2, App1
15	1778.5	79.8	431	1	US-08-381-433A-2	Sequence 2, App1
16	1776.5	79.7	431	4	US-09-799-978-20	Sequence 20, App1
17	1770.5	79.4	431	3	US-08-981-189B-11	Sequence 11, App1
18	1770.5	79.4	431	3	US-08-48-746-10	Sequence 10, App1
19	1770.5	79.4	431	3	US-09-580-734-10	Sequence 10, App1
20	1770.5	79.4	431	4	US-08-374-009-10	Sequence 10, App1
21	1770.5	79.4	431	4	US-09-191-724-10	Sequence 24, App1
22	1770.5	79.4	431	4	US-09-799-978-24	Sequence 26, App1
23	1779	79.4	430	4	US-09-799-978-26	Sequence 26, App1
24	1582.5	71.0	428	4	US-09-799-978-36	Sequence 36, App1
25	1582	70.8	420	4	US-09-799-978-42	Sequence 42, App1
26	1582.5	70.8	445	4	US-09-799-978-34	Sequence 34, App1
27	1566	70.3	415	1	US-08-110-286A-2	Sequence 2, App1

## ALIGNMENTS

RESULT 1  
US-09-799-978-32  
; Sequence 32, Application US/09799978

; Patent No. 6670140  
; GENERAL INFORMATION:

; APPLICANT: The Procter & Gamble Company

; APPLICANT: Sheldan, Russell  
; TITLE OF INVENTION: Methods for Identifying Compounds for Regulating Muscle Mass or Factor Receptors

; TITLE OF INVENTION: Method for Identifying Compounds for Regulating Muscle Mass or Factor Receptors

; FILE REFERENCE: 8448

; CURRENT APPLICATION NUMBER: US/09/799,978

; NUMBER OF SEQ ID NOS: 44

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO: 32

; LENGTH: 413

; TYPE: PRT

; ORGANISM: Xenopus laevis

US-09-799-978-32

Query Match 100.0% ; Score 2229; DB 4; Length 413;

Best Local Similarity 100.0% ; Pred. No. 1.2e-200; Matches 413; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MDSTIPEIIDEPDANCSSLDAFDQDFDANSCLLDAFDOSFLHSSSSPSSFFEGPYCSATIDQIGNCWPSLAG 60  
Db 1 MDSTIPEIIDEPDANCSSLDAFDQDFDANSCLLDAFDOSFLHSSSSPSSFFEGPYCSATIDQIGTCWPSLAG 60

Qy 1 MDSTIPEIIDEPDANCSSLDAFDQDFDANSCLLDAFDOSFLHSSSSPSSFFEGPYCSATIDQIGTCWPSLAG 60  
Db 1 MDSTIPEIIDEPDANCSSLDAFDQDFDANSCLLDAFDOSFLHSSSSPSSFFEGPYCSATIDQIGTCWPSLAG 60

Qy 1 ELVERPDPDSENGIRNTTRVYRECENGFTWASHWNNYSOCYVPILDNKRKYALHYKIALI 120  
Db 1 ELVERPDPDSENGIRNTTRVYRECENGFTWASHWNNYSOCYVPILDNKRKYALHYKIALI 120

Qy 1 INYLGHCISILALVIAFLFLCLRSIRCLRNLIHMLALITTEILRNIMWFLLOMIDANIHE 180  
Db 1 INYLGHCISILALVIAFLFLCLRSIRCLRNLIHMLALITTEILRNIMWFLLOMIDANIHE 180

Qy 1 SNEBWRCITIINYFVTFNFWMFYEGCYLHTATWNTYSTDKLKRKVFLFICWICPSPI 240  
Db 1 SNEBWRCITIINYFVTFNFWMFYEGCYLHTATWNTYSTDKLKRKVFLFICWICPSPI 240

Qy 1 TSETIQRKAVATLVLPLGLITYLFFVNQGEDDVSIQIVIYFSPLQSTQFFYVF 360  
Db 1 TSETIQRKAVATLVLPLGLITYLFFVNQGEDDVSIQIVIYFSPLQSTQFFYVF 360

Qy 1 IVTWAIKLFYNEQWIGKEPKGYIDYQGRVLVLLINFVLENVRLMTKLRAST 300  
Db 1 IVTWAIKLFYNEQWIGKEPKGYIDYQGRVLVLLINFVLENVRLMTKLRAST 300

Qy 1 TSETIQRKAVATLVLPLGLITYLFFVNQGEDDVSIQIVIYFSPLQSTQFFYVF 360  
Db 1 TSETIQRKAVATLVLPLGLITYLFFVNQGEDDVSIQIVIYFSPLQSTQFFYVF 360

Qy 1 YCFLNGEVRSAAKWRHRDHSLRVARAMSIPSPTRISFSIKQTAAV 413  
Db 1 YCFLNGEVRSAAKWRHRDHSLRVARAMSIPSPTRISFSIKQTAAV 413

RESULT 2  
US 09-799-979-38  
Sequence 38, Application US/09799978  
Patent No. 6670140  
GENERAL INFORMATION:  
APPLICANT: The Procter & Gamble Company  
APPLICANT: Isfort, Sheldon, Russell  
TITLE OF INVENTION: Methods for Identifying Compounds for Regulating Muscle Mass or Function Using Corticotropin Releasing Factor Receptors  
TITLE OF INVENTION: Function Using Corticotropin Releasing Factor Receptors  
CURRENT APPLICATION NUMBER: US/09/799,978  
FILE REFERENCE: 8448  
CURRENT FILING DATE: 2001-03-06  
NUMBER OF SEQ ID NOS: 44  
SEQ ID NO: 38  
LENGTH: 405  
TYPE: PRT  
ORGANISM: *Amelurus nebulosus*  
US 09-799-978-38

Query Match 81.1%; Score 1807; DB 4; Length 405;  
Best Local Similarity 79.9%; Pred. No. 4e-161;  
Matches 330; Conservative 33; Mismatches 42; Indels 8; Gaps 2;

Query 1 MDSTFEIIDEFDANCSLLDAFDPSLISESSSEFFGPGPSATIDQIGTCWPRSLA 60  
1 MEVSLIELI--SVEVNCSLADAFGDPAYNSDAL-----YCNAATADEIGTCWPRSGA 52  
61 ELVERPCPPDSFNGIRNTNVRTRVRECNGTWASWMYNSQCVPLDNRKRYAHYKIAL 120  
53 RVVARPCPDINGKYNSTSAVTCLENGTWARKINTSCEPFLERKRYPHKALI 112  
124 INYLGHCISLALVIAFLFLCLRSIRCLRNIIHWNLTTEFLRNIMMFLQIDNTHE 180  
113 INYLGHCISVGALVTAFLFLCLRSIRCLRNIIHWNLTTEFLRNIMMFLQIDNTHE 172  
184 SNEWCRCITIINFVNFNMVEGGYLTAIIWMTSTDKRKWFLFLGWCICSP 240  
173 RNEPNCRLITVNVYFVNTNFNMVEGGYLTAIIWMTSTDKRKWFLFLGWCICP 232

Query 241 IWTWAIKFLFYENEQWIGKEPGKTYIDYIYQGRVYLVLLINFVNLTRMLTKRAS 300  
233 IIWAVGRLNNECWFGEPEGPVYDYLIGMLFLGTYMLFVNPQGDDVSIYFVNLTRMLTKRAS 292  
301 TSETIQRKAVAKATVLLPLIGTYMLFVNPQGDDVSIYFVNLTRMLTKRAS 360  
293 TSETIQRKAVAKATVLLPLIGTYMLFVNPQGDDVSIYFVNLTRMLTKRAS 352

Query 361 YCFINGEVSAARKWHRQDHHSIRVVARANSIPTSTRISPHSIKOTAAV 413  
353 YCFINGEVSAVKWHRQDHHSIRVVARANSIPTSTRISPHSIKOTAAV 405

RESULT 3  
US 09-631-603-12  
Sequence 12, Application US/09631603  
Patent No. 6733930  
GENERAL INFORMATION:  
APPLICANT: Hodge, Martin R.  
APPLICANT: Lloyd, Clare  
APPLICANT: Weich, Nadine  
TITLE OF INVENTION: 15571, A No. 6733930el GPCR-like Molecule of the Secretin-Like Family and Uses Thereof  
FILE REFERENCE: 5800-48A  
CURRENT APPLICATION NUMBER: US/09/631,603  
CURRENT FILING DATE: 2000-08-03  
PRIOR APPLICATION NUMBER: 09-515,781  
PRIOR FILING DATE: 2000-02-29  
SEQUENCE: FastSEQ for Windows Version 3.0  
SEQ ID NO: 12  
LENGTH: 411  
TYPE: PRT  
ORGANISM: *Homo sapiens*  
US-09-631-603-12

Query Match 80.9%; Score 1804; DB 4; Length 411;  
Best Local Similarity 80.0%; Pred. No. 7.7e-161;  
Matches 333; Conservative 33; Mismatches 42; Indels 8; Gaps 4;

Query 1 MDSTFEIIDEFDANCSLLDAFDPSLHSESSSEFFGPGPSATIDQIGTCWPRSL 58  
1 MDALALHSLL--EANCSL-ALAELLUDGNGPPLDPEPGPSYCTTLDQIGTCWPRSA 55  
59 AGELVERPCPDSNGIYNTNVRVRECNGTWASWMYNSQCVPLDNRKRYAHYK 117  
56 AGALVERPCPPEFNGIYNTNVRVRECNGTWASKINYNSQCEPFLDDKQRKYDHYR 115  
118 ALIINYLGHCISLALVIAFLFLCLRSIRCLRNIIHWNLTTEFLRNIMMFLQIDN 177  
116 ALVNVYLGHCISVAALVAAFLFLCLRSIRCLRNIIHWNLTTEFLRNIMMFLQIDV 175

Query 178 IHESNNEWCRCITIINYKVTNFNMVEGGYLTAIIWMTSTDKRKWFLFLGWCICP 237  
176 VHESNNEWCRCITIINYKVTNFNMVEGGYLTAIIWMTSTERLKCHFLGWCICP 235

Query 238 SPLITVWAIKFLFYENEQWIGKEPGKTYIDYIYQGRVYLVLLINFVNLTRMLTKR 297  
236 FPIVAVAGKLYYENQWCFGEKEPFLDVIYQGPVIIWMTSTDKRKWFLFLGWCICP 295

Query 298 ASTSETIQRKAVAKATVLLPLIGTYMLFVNPQGDDVSIYFVNLTRMLTKRAS 357  
296 ASTSETIQRKAVAKATVLLPLIGTYMLFVNPQGDDVSIYFVNLTRMLTKRAS 355

RESULT 4  
Sequence 8, Application US/08381433A  
Patent No. 5786203  
GENERAL INFORMATION:  
APPLICANT: Lovenberg, Timothy W.  
APPLICANT: Oltersdorf, Tillman  
APPLICANT: Liaw, Chen  
APPLICANT: Grigoriadis, Dimitri E.  
APPLICANT: DeSouza, Errol B.  
TITLE OF INVENTION: CORTICOTROPIN RELEASING FACTOR 2  
TITLE OF INVENTION: CORTICOTROPIN RELEASING FACTOR 2  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SEED and BERRY  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: USA  
ZIP: 98104-7092  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/381,433A  
FILING DATE: 31-JAN-1995  
CLASS/CAUTION: 435  
ATTORNEY/AGENT INFORMATION:

NAME: McMasters, David D.  
 REGISTRATION NUMBER: 33,963  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (206) 622-4910  
 TELEX: (206) 682-6031  
 INFORMATION FOR SEQ ID NO: 8:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 411 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-381-43A-8

Query Match Score 80.7% Score 1799, DB 1; Length 411;  
 Best Local Similarity 79.8% Pred. No. 2, 3e-160;  
 Matches 332; Conservative 33; Mismatches 43; Indels 8; Gaps 4;

Qy 1 MDSTIFELIDEFDANCISLLDAFQDSFLHSESSSSFFGFFGP--YCSATIDQIGTCWPRSL 58  
 Db 1 MDAALLHSLL--EANCSL--ALAEELLQDGGPPLDPFGSYNSCTTLDIGTCWPRSL 55

Qy 59 AGELVERPCPDSPNGYRNTTRNVRCPFENGTWASWMNYSQCPVPLDNCN-KRYALHYKI 117  
 Db 56 AGALVERPCPEYNGYKNTTRNATRAECLNGTWASKINYSQCEPILDDKQRKYDLYRI 115

Qy 118 ALINYLGHCISLALVIAFLFLCLRSIRCLRNITIHWNLITTFILRNWFLQDHN 177  
 Db 116 ALVNVYLGHCVSAALVBAFLFLALRSIRCLRNITIHWNLITTFILRNWFLQDHN 175

Qy 178 IHESENWCRCTTINYFVVTNFNFVEGCYLHTAVTMYSTDLKRYVFLFCWICP 237  
 Db 176 VHESENWCHCITINYFVVTNFNFVEGCYLHTAVTMYSTDLKRYVFLFCWICP 235

Qy 238 SPLITWAIKLCFLYNEQCGWIGKEPKYIDYIYQGRVILVILNFLENVRLIMTKL 297  
 Db 236 EPIIVAWAIGKLYYNEOCWNGKEPDLDVYIYQGPFLVILNFLENVRLIMTKL 295

Qy 298 ASTTSETIQRKAVATLVLPLGTTMLPFVNPGEDDVSIQVYFNSPLQSGQPFV 357  
 Db 296 ASTTSETIQRKAVATLVLPLGTTMLPFVNPGEDDVSIQVYFNSPLQSGQPFV 355

Qy 358 SVFYCFLNGEVRSAAKWRWQDHSLRVYARAMSPTSPTRISFHSIKOTAIV 413  
 Db 356 SVFYCFLNGEVRSAAKWRWQDHSLRVYARAMSPTSPTRISFHSIKOTAIV 411

Qy 367 RESULT 6  
 Db 368 US-09-881-401-8  
 ; Sequence 8, Application US/09881401  
 ; Patent No. 6723841  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Lovensberg, Timothy W.  
 ; Laiaw, Chen  
 ; Grigoriadis, Dimitri E.  
 ; Chalmers, Derek T.  
 ; DeSouza, Errol B.  
 ; TITLE OF INVENTION: CORTICOTROPIN RELEASING FACTOR 2  
 ; NUMBER OF SEQUENCES: 8  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Seed Intellectual Property Law Group  
 ; STREET: 701 Fifth Avenue, Suite 6300  
 ; CITY: Seattle  
 ; STATE: Washington  
 ; COUNTRY: USA  
 ; ZIP: 98104-7092  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: floppy disk  
 ; COMPUTER: IBM PC Compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent in Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/881,401  
 ; FILING DATE: 13-Jun-2001  
 ; CLASSIFICATION: <Unknown>  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Christiansen, William T.  
 ; REGISTRATION NUMBER: 44,614  
 ; REFEERENCE/DOCKET NUMBER: 690068-401C4  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (206) 622-4900  
 ; TELEFAX: (206) 682-6031  
 ; INFORMATION FOR SEQ ID NO: 8:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 411 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 8:

RESULT 5  
 US-09-799-978-10  
 ; Sequence 10, Application US/09799978  
 ; Patent No. 6767040  
 ; GENERAL INFORMATION:  
 ; APPLICANT: The Procter & Gamble Company  
 ; APPLICANT: Isfort, Robert  
 ; APPLICANT: Sheldon, Russell  
 ; TITLE OF INVENTION: Methods for Identifying Compounds for Regulating Muscle Mass or Function Using Corticotropin Releasing Factor Receptors  
 ; CURRENT APPLICATION NUMBER: US/09/799,978  
 ; CURRENT FILING DATE: 2001-03-06  
 ; NUMBER OF SEQ ID NOS: 44  
 ; SOFTWARE: Patent version 3.0  
 ; FILE REFERENCE: 8448  
 ; CURRENT APPLICATION NUMBER: US/09/799,978  
 ; SEQ ID NO 10  
 ; LENGTH: 411  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; US-09-799-978-10

Query Match Score 80.7% Score 1799, DB 4; Length 411;  
 Best Local Similarity 79.8% Pred. No. 2, 3e-163;  
 Matches 332; Conservative 33; Mismatches 43; Indels 8; Gaps 4;



TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 858-552-1311  
 TELEFAX: 858-552-0095  
 INFORMATION FOR SEQ ID NO: 12:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 411 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 FEATURE:  
 NAME/KEY: Protein  
 LOCATION: 1..411  
 OTHER INFORMATION: /note= "Rat CRF-R2 Short Form"  
 PUBLICATION INFORMATION:  
 AUTHORS: Lovendberg, Timothy W  
 AUTHORS: Liaw, Chen W  
 AUTHORS: Grigoriadis, Dimitri E  
 AUTHORS: Cleverger, William  
 AUTHORS: Chalmers, Derek T  
 AUTHORS: Desouza, Errol B  
 AUTHORS: Otersdorf, Tillman  
 TITLE: Cloning and characterization of a  
 functionally distinct corticotropin-releasing  
 factor receptor subtype from rat brain  
 JOURNAL: Proc. Natl. Acad. Sci. U.S.A.  
 VOLUME: 92  
 PAGES: 836-840  
 DATE: January-1995  
 US-08-981-189B-12

Query Match 80.4%; Score 1793; DB 3; Length 411;  
 Best Local Similarity 80.0%; Pred. No. 8.3e-160;  
 Matches 333; Conservative 30; Mismatches 45; Indels 8; Gaps 4;

Qy 1 MDSTIFFRIIIDEFDANGSLLDAFDQSTLHSSESSFFGPEGP--YCSATIDQIGTCWPRSL 58  
 Db 1 MDAA---LLSLLNEANCSL--ALAEELLGGEPPPEGPSYCNTTLDQIGTCWPSA 55

Qy 59 AGELEYVERPCPDSENGIRYNTTRAVYRECENGNTWASWMMYNSQCVPLDNNK-RKYALHYKI 117  
 Db 56 PGALVERPCPEYNGKNTTRAVYRECENGNTWASRINYSHCEILDDQKRYDHRYI 115

Qy 118 ALINNYLGHCSISLALVIAPIALFLCLRSIRCLRNTHWNLITTPILRNWMLQDIDHN 177  
 Db 116 ALINNYLGHCVSVALYAAFLFLPLVPSIRCLRNTHWNLITTPILRNWMLQDIDHE 175

Qy 178 IHESEWVWCRCITTYNYFVTTNFPMVFGCYLTTAIVNTYSTDLRKWVFLFGWCIP 237  
 Db 176 VHEGNEWVWCRCVTTNFPMVFGCYLTTAIVNTYSTDLRKWVFLFGWCIP 235

Qy 238 SPTIVTWAICKFLYENEQCIGKEPKYIDIXYQGRVILNLNFELNVRILMTKL 297  
 Db 236 CPIIVAWAVGKLYYNEQCMWFGKEQCDLVDIXYQCPPLILVLLNFELNVRILMTKL 295

Qy 298 ASTTSETIQRKAVATVLLPLIGITYMUFFNGEDVSIQVITYFNSFLOSSQGFFV 357  
 Db 296 ASTTSETIQRKAVATVLLPLIGITYMUFFNGEDDLSQIVYFNSFLOSSQGFFV 355

Qy 358 SVFYCYLNGEVRSALARWKWRHRWQDHSLRYTVARAMSIPSPTRSFHSIKQTAAV 413  
 Db 356 SVFYCFENGEVRSALARWKWRHRWQDHSLRYTVARAMSIPSPTRSFHSIKQTAAV 411

RESULT 10  
 US-09-881-401-4  
 Sequence 4, Application US/09881401  
 Patent No. 6723841  
 GENERAL INFORMATION:  
 APPLICANT: Lovenberg, Timothy W.  
 Otersdorf, Timan  
 Liaw, Chen  
 Grigoriadis, Dimitri E.  
 Chalmers, Derek T.  
 DeSouza, Errol B.  
 TITLE OF INVENTION: CORTICOTROPIN RELEASING FACTOR 2  
 NUMBER OF SEQUENCES: 8  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Seed Intellectual Property Law Group  
 STREET: 701 Fifth Avenue, Suite 6300  
 CITY: Seattle  
 STATE: Washington  
 COUNTRY: USA  
 ZIP: 98104-7092  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC Compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/881,401  
 FILING DATE: 13-Jun-2001

RESULT 9  
 US-09-799-978-18  
 Sequence 18, Application US/09799978  
 Patent No. 6670140  
 GENERAL INFORMATION:  
 APPLICANT: The Procter & Gamble Company  
 APPLICANT: Isfort, Robert  
 APPLICANT: Sheldon, Russell  
 TITLE OF INVENTION: Methods for Identifying Compounds for Regulating Muscle Mass or Function Using Corticotropin Releasing Factor Receptors  
 TITLE OF INVENTION: Function Using Corticotropin Releasing Factor Receptors

CLASSIFICATION: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Christiansen, William T.

REGISTRATION NUMBER: 44 614

REFERENCE/DOCKET NUMBER: 690068 .401C4

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206) 622-4900

TELEFAX: (206) 682-6031

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 411 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 4:

US-09-881-401-4

Query Match 80.4%; Score 1793; DB 4; Length 411;

Best Local Similarity 80.0%; Pred. No. 8.3e-160;

Matches 333; Conservative 30; Mismatches 45; Indels 8; Gaps 4;

Qy 1 MDSTIFELIIDEFDANCSLIDAQDFSEISSLSSFFGFFGP- YCSATIDQIGCWPRLS 58

Db 1 MDAA--LISLLEANCSL--ALABELLIDLGWGPBDPPGSPYSCNTIDQIGTCWPSSA 55

Qy 59 AGEIVERPCPDSENGIRNTTRVYRECENGITWASMMYSCYCPILDKN-RKEYALHYK 117

Db 56 PGALVERPCPBEYNGIKYNTTRNAYRECENGITWASRITYSHSCPBDKQRYDLHYR 115

Qy 118 ALIINYLGHCISIALLYATIPLFLCLSRCLRNTHWLLTFLRNMFLLQIDH 177

Db 116 ALIINYLGHCISVVALVAAPFLFLVRSIICRLRNTHWLLTFLRNMFLLQIDH 175

Qy 178 IHESNFWCRCTTIIYFVTTNFMMFVEGCVLHTATIYTSTDKLRKWFPLIGWCIP 237

Db 176 VHEGNEFWCRCTVTFNYFVTTNFMMFVEGCVLHTATIYTSTEHRLKWFPLIGWCIP 235

Qy 238 SPIITVWAICKLFYNEQCMGKPGKYIDYIYQGRVILVLLNFVFVNLVRLMTKL 297

Db 236 CPIIYAWAVGKLYYNEQCMGKPGKYDLYIYQGRVILVLLNFVFVNLVRLMTKL 295

Qy 298 ASTTSETTIVRKAVATLVLPLLIGITYMLFFVNGEDDVSQIVYIYENFSQFQFV 357

Db 296 ASTTSETTIVRKAVATLVLPLLIGITYMLFFVNGEDDVSQIVYIYENFSQFQFV 355

Qy 358 SVFYCPLNGEVRSARKRWHRWDHSLRVARAMSISPTSPTRISFHSIKQPAAV 413

Db 356 SVFYCPLNGEVRSARKRWHRWDHSLRVARAMSISPTSPTRISFHSIKQPAAV 411

RESULT 11

US-09-799-978-14

Query Match 80.1%; Score 1786; DB 4; Length 438;

Best Local Similarity 82.3%; Pred. No. 4.1e-159;

Matches 325; Conservative 31; Mismatches 35; Indels 4; Gaps 3;

Qy 45 ALIEQYCH-IMPLTNLSPSYCNCNTTDQIGTCWPSSAAGLVERPCPEYNGKNTT 103

Db 46 AFQDFSLHSESSSFFGFFGP--YCSATIDQIGTCWPRLSLAGELVERPCPDSENGIRNTT 79

Qy 80 RNTYRECENGITWASMMYSCYCPILDKN-RKEYALHYKIALIINLGHCISIILALVIAFL 138

Db 104 RNAFRECLENGTIVASKINYSQCPBLDKQRYDLHYTALVYNNLGHCVSVAALVAAPL 163

Qy 139 LFLCLRSRCLRNTHWLLTFLRNMFLLQIDHNTIHNESNEWCRCTTINYFV 198

Db 164 LFLALRSRCLRNTHWLLTFLRNMFLLQIDHNTIHNESNEWCRCTTINYFV 223

Qy 199 TNFFWMFVEGCVLHTATVYSTDKLRKWFPLIGWCIPSP1LTWAIKLFYENEQCWI 258

Db 224 TNFFWMFVEGCVLHTATVYSTERLRKCLFLFGWCIPSP1IVAWAIGKLYYNEQCMW 283

Qy 259 GKEPKYIDYQGRVILVLLTFLNIVRLMTKLRASTTSETIYRKAVATLVL 318

Query Match 80.2%; Score 1787.5; DB 4; Length 397;

Best Local Similarity 85.4%; Pred. No. 2.6e-159;

US-08-981-189B-13

Query Match 80.1%; Score 1784.5; DB 3; Length 431;

Best Local Similarity 85.5%; Pred. No. 5.5-159; Mismatches 24;

Matches 324; Conservative 24; Indels 3; Gaps 2

Qy 38 FEGP-YCSATIDQGTCTWRSLASGELEYENCPDPFGTIVNTTNYTRECENGTMWAS 95

Db 53 FSGPYSYCNLTDQGTCTWPSAPEGVCPPEYNGIKNTTNYRECENGTMWAS 112

Qy 96 MNYSQCVPLDNK-RKAYHQLALINYGHCSIALVATPLFLCLSRCLRNTH 154

Db 113 INVSCEPILDDKQKDYLDHYRALLINVLGHCVSVVALVRAFLFLVLSRCLRNTH 172

Qy 155 WNLITTFILERNMWFQMLQIDHNIHESNEYWCRCTTIIYMFVVTNFWMFVEGYLHTA 214

Db 173 WNLITTFILERNITWFQLDQGTCTWPSAPEGVCPPEYNGIKNTTNYRECENGTMWAS 232

Qy 215 IVMTSTDKLWKWFLPIFGCIPSPVITWACKLYFENEQCGWIGEKGPKYDVTQGRV 274

Db 233 IVMTSTEHRLWKWFLPIFGCIPCPVAVGKLYFENEQCGWIGEKGPKDLYDVTQGP 292

Qy 275 ILVLLINFVFLNIRILMVKLRASTTSETIQYRKAVALVLLPLGLITMLFVFNPG 334

Db 293 ILVLLINFVFLNIRILMVKLRASTTSETIQYRKAVALVLLPLGLITMLFVFNPG 352

Qy 335 DDVSQIVFVYENFSFLQSGQGFVSYFVCFNGEVSAARKKWRHWDHSLRVRVARAMS 394

Db 353 DDLSQIVFVYENFSFLQSGQGFVSYFVCFNGEVSAALKWRHWDHSLRVRVARAMS 412

RESULT 14

US-08-981-189B-13

Sequence 13, Application US/08981-189B

Patent No. 6214797

GENERAL INFORMATION:

APPLICANT: UROCORTIN PEPTIDES

NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESS:

ADDRESSEE: FITCH, EVEN, TABIN & FLANNERY

STREET: 120 S. LaSalle Street, Suite 1600

CITY: Chicago

STATE: Illinois

COUNTRY: USA

ZIP: 60603

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/981-189B

FLILING DATE: 10-DEC-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/028,144

FLILING DATE: 13-TUN-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/002,223

FLILING DATE: 11-AUG-1995

ATTORNEY/AGENT INFORMATION:

NAME: Schumann, James J.

REGISTRATION NUMBER: 20,856

REFERENCE/DOCKET NUMBER: 57611

TELECOMMUNICATION INFORMATION:

TELEPHONE: 858-552-1311

TELEFAX: 858-552-0095

INFORMATION FOR SEQ ID NO: 13:

SEQUENCE CHARACTERISTICS:

LENGTH: 431 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

FEATURE:

NAME/KEY: Protein

LOCATION: 1..431

OTHER INFORMATION: /note= "Rat CRF-R2 Long Form"

PUBLICATION INFORMATION:

AUTHORS: Lovenberg, Timothy W

AUTHORS: Liaw, Chen W

AUTHORS: Grigoriadis, Dimitri E

AUTHORS: Cleverger, William

AUTHORS: Chalmers, Derek T

AUTHORS: Desouza, Errol B

AUTHORS: Oltersdorff, Tilmann

AUTHORS: Cloning and characterization of a functionally distinct corticotropin releasing factor receptor subtype from rat brain

JOURNAL: Proc. Natl. Acad. Sci. U.S.A.

VOLUME: 92

PAGES: 836-840

DATE: January-1995

Query Match 80.1%; Score 1784.5; DB 3; Length 431;

Best Local Similarity 85.5%; Pred. No. 5.5-159; Mismatches 24;

Matches 324; Conservative 24; Indels 3; Gaps 2

Qy 38 FEGP-YCSATIDQGTCTWRSLASGELEYENCPDPFGTIVNTTNYTRECENGTMWAS 95

Db 53 FSGPYSYCNLTDQGTCTWPSAPEGVCPPEYNGIKNTTNYRECENGTMWAS 112

Qy 96 MNYSQCVPLDNK-RKAYHQLALINYGHCSIALVATPLFLCLSRCLRNTH 154

Db 113 INVSCEPILDDKQKDYLDHYRALLINVLGHCVSVVALVRAFLFLVLSRCLRNTH 172

Qy 155 WNLITTFILERNMWFQMLQIDHNIHESNEYWCRCTTIIYMFVVTNFWMFVEGYLHTA 214

Db 173 WNLITTFILERNITWFQLDQGTCTWPSAPEGVCPPEYNGIKNTTNYRECENGTMWAS 232

Qy 215 IVMTSTDKLWKWFLPIFGCIPSPVITWACKLYFENEQCGWIGEKGPKYDVTQGRV 274

Db 233 IVMTSTEHRLWKWFLPIFGCIPCPVAVGKLYFENEQCGWIGEKGPKDLYDVTQGP 292

Qy 275 ILVLLINFVFLNIRILMVKLRASTTSETIQYRKAVALVLLPLGLITMLFVFNPG 334

Db 293 ILVLLINFVFLNIRILMVKLRASTTSETIQYRKAVALVLLPLGLITMLFVFNPG 352

Qy 335 DDVSQIVFVYENFSFLQSGQGFVSYFVCFNGEVSAARKKWRHWDHSLRVRVARAMS 394

Db 353 DDLSQIVFVYENFSFLQSGQGFVSYFVCFNGEVSAALKWRHWDHSLRVRVARAMS 412

RESULT 14

US-09-881-401-2

Sequence 2, Application US/09881401

Patent No. 6723841

GENERAL INFORMATION:

APPLICANT: Lovenberg, Timothy W.

ATTORNEY/AGENT INFORMATION:

Oltersdorff, Tilmann

Liaw, Chen

Grigoriadis, Dimitri E.

Chalmers, Derek T.

Desouza, Errol B.

TELEPHONE: 206-622-4900

TITLE OF INVENTION: CORTICOTROPIN RELEASING FACTOR 2

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:

OPERATING SYSTEM: PC-DOS/MS-DOS

OPERATOR: IBM PC compatible

SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

ADDRESSSEE: Seed Intellectual Property Law Group

STREET: 701 Fifth Avenue, Suite 6300

CITY: Seattle

STATE: Washington

COUNTRY: USA

ZIP: 98104-7092

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

OPERATOR: IBM PC compatible

SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/881,401

FILING DATE: 13-Jun-2001

CLASIFICATION: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Christiansen, William T.

REGISTRATION NUMBER: 44,614

REFERENCE/DOCKET NUMBER: 650068-401C4

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206) 622-4900

TELEFAX: (206) 622-6031

INFORMATION FOR SEQ ID NO: 2:

PAGES: 2

SEQUENCE CHARACTERISTICS:  
 LENGTH: 431 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
 US-09-881-401-2

Query Match 80.1%; Score 1784.5; DB 4; Length 431;  
 Best Local Similarity 85.5%; Pred. No. 5.5e-159;  
 Matches 324; Conservative 24; Nismatches 28; Indels 3; Gaps 2;

Query 38 FEGP--YCSATIDQIGTCWPRSLAGELVLPQPCPDSENGTRYNTRVBCPFENGTWASW 95  
 Db 53 FSGPVSYCNLTQDQIGTCWPSQAPALIVRBCPPEVNGKYNTRVBCPFENGTWASR 112  
 Qy 96 MNYSQCVPLDNNK-RKYALHYKIALIINTLGHCTISLALVIAFLFLCLRSIRCRNTH 154  
 Db 113 INYSHCEPLDQKRYDLYRIALIINTLGHCVSVALVAAPFLFLVRSIRCRNTH 172  
 Qy 155 WNLITPFLRNIMMFLQIMDHNHESNEWCRCITTTIYKNTWNEFMEVEGCCYLTIA 214  
 Db 173 WNLITPFLRNITWFLQIDHEVNEGNEYWCRCVTTIENXYFVYTNEFWMFVEGCCYLTIA 232  
 Qy 215 IVMTYSTDQKRWFLDIFGMCICPSPLIVTAICKLYFEVNEQCWIGKEPKYIDVYQGV 274  
 Db 233 IVMYSTEHLRKWLFLIGMCICPSPLIVTAICKLYFEVNEQCWIGKEPKYIDVYQGV 292  
 Qy 275 ILVLLINFVFLNIVRLIMTKLRASTTSETIQRKAVATLVLPLLGITMLFFVNPG 334  
 Db 293 ILVLLINFVFLNIVRLIMTKLRASTTSETIQRKAVATLVLPLLGITMLFFVNPG 352  
 Qy 335 DDVSQIVPVIYNSPLSFGFVFSVYCFENGTPSAARKRWHQDHISLRVVARAMS 394  
 Db 353 DDLSQLVFTENSF-LQSFGFVFSVYCFNGEVRSALRERWHRQDHALRVPVARAMS 412  
 Qy 395 IPTSPRISIHSIKQTAAV 413  
 Db 413 IPTSPRISIHSIKQTAAV 431

RESULT 15-US-08-381-433A-2  
 Sequence 2, Application US/08381433A  
 Patent No. 5786203

GENERAL INFORMATION:  
 APPLICANT: Lovenberg, Timothy W.  
 APPLICANT: Otersdorf, Tilmann  
 APPLICANT: Liaw, Chen  
 APPLICANT: Grigoriadis, Dimitri E.  
 APPLICANT: Desouza, Errol B.  
 TITLE OF INVENTION: CORTICOTROPIN RELEASING FACTOR 2  
 TITLE OF INVENTION: RECEPTORS  
 NUMBER OF SEQUENCES: 8  
 CORRESPONDENCE ADDRESS:  
 STREET: 6300 Columbia Center, 701 Fifth Avenue  
 CITY: Seattle  
 STATE: Washington  
 COUNTRY: USA  
 ZIP: 98104-7092

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC Compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/381,433A  
 FILING DATE: 31-JAN-1995  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: McMasters, David D.  
 REGISTRATION NUMBER: 33,963

REFERENCE/DOCKET NUMBER: 690068.401C1  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (206) 622-4900  
 TELEFAX: (206) 682-6031  
 TELEX: 3723836 SEEDNDBERRY  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 431 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-381-433A-2

Query Match 79.8%; Score 1778.5; DB 1; Length 431;  
 Best Local Similarity 85.2%; Pred. No. 2e-158;  
 Matches 323; Conservative 24; Nismatches 29; Indels 3; Gaps 2;

Qy 38 FEGP--YCSATIDQIGTCWPRSLAGELVLPQPCPDSENGTRYNTRVBCPFENGTWASW 95  
 Db 53 FSGPVSYCNLTQDQIGTCWPSQAPALIVRBCPPEVNGKYNTRVBCPFENGTWASR 112  
 Qy 96 MNYSQCVPLDNNK-RKYALHYKIALIINTLGHCTISLALVIAFLFLCLRSIRCRNTH 154  
 Db 113 INYSHCEPLDQKRYDLYRIALIINTLGHCVSVALVAAPFLFLVRSIRCRNTH 172  
 Qy 155 WNLITPFLRNIMMFLQIMDHNHESNEWCRCITTTIYKNTWNEFMEVEGCCYLTIA 214  
 Db 173 WNLITPFLRNITWFLQIDHEVNEGNEYWCRCVTTIENXYFVYTNEFWMFVEGCCYLTIA 232  
 Qy 215 IVMTYSTDQKRWFLDIFGMCICPSPLIVTAICKLYFEVNEQCWIGKEPKYIDVYQGV 274  
 Db 233 IVMYSTEHLRKWLFLIGMCICPSPLIVTAICKLYFEVNEQCWIGKEPKYIDVYQGV 292  
 Qy 275 ILVLLINFVFLNIVRLIMTKLRASTTSETIQRKAVATLVLPLLGITMLFFVNPG 334  
 Db 293 ILVLLINFVFLNIVRLIMTKLRASTTSETIQRKAVATLVLPLLGITMLFFVNPG 352  
 Qy 335 DDVSQIVPVIYNSPLSFGFVFSVYCFENGTPSAARKRWHQDHISLRVVARAMS 394  
 Db 353 DDLSQLVFTENSF-LQSFGFVFSVYCFNGEVRSALRERWHRQDHALRVPVARAMS 412  
 Qy 395 IPTSPRISIHSIKQTAAV 413  
 Db 413 IPTSPRISIHSIKQTAAV 431

Search completed: August 20, 2005, 00:38:08  
 Job time : 45 secs

GenCore version 5.1.6  
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Run on: August 20, 2005, 00:09:52 ; Search time 166 Seconds  
 (without alignments)  
 962,241 Million cell updates/sec

Title: US-10-649-852-32  
 Perfect score: 2229  
 Sequence: 1 MDSTIPEIIIDEFDANCSLLI.....SIPISPRISFHSIKQTAAV 413

Scoring table: BLOSUM62  
 Gapop 10.0 , Gapext 0.5

Sequences: 2105692 seqs, 386760381 residues

Searched: Total number of hits satisfying chosen parameters: 2105692

מִתְּנִשְׁאָלָה בְּנֵי יִשְׂרָאֵל וְנִשְׁאָלָה בְּנֵי כָּל־עַמִּים.

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Summary 45 summaries

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Database : A_Geneseq_16Dec04:*
 1: GeneseqP1980s:*
 2: GeneseqP1990s:*
 3: GeneseqP2000s:*
 4: GeneseqP2001s:*
 5: GeneseqP2002s:*
 6: GeneseqP2003as:*
 7: GeneseqP2003bs:*

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No. is the number of results predicted by chance to have a score greater than or equal to the score of the total distribution. It is derived by analysis of the total score distribution.

סימן

Result No.	Score	Query	Match	Length	DB	ID	
		Start	End	Count	Score	Start	End
1	22229	100.0	4113	5	AA01		
2	22229	100.0	4113	8	AD05		
3	1807	81.1	405	5	AA01		
4	1807	81.1	405	8	AD05		
5	1804	80.9	411	2			
6	1804	80.9	411	4	AAB7		
7	1804	80.9	411	7	ADC5		
8	1804	80.9	411	8	AD02		
9	1799	80.7	411	2	AA09		
10	1799	80.7	411	5	AA01		
11	1799	80.7	411	6	ABP8		
12	1799	80.7	411	8	AD05		
13	1799	80.7	411	8	AD02		
14	1793	80.4	411	2	ABU6		
15	1793	80.4	411	5	AA01		
16	1793	80.4	411	8	AD05		
17	1790	80.3	411	2	AA09		
18	1787.5	80.2	397	5	AA01		
19	1787.5	80.2	397	8	AD05		
20	1786	80.1	438	5	AA01		
21	1786	80.1	438	8	AD05		
22	1784.5	80.0	431	2	ABU5		
23	1776.5	79.7	431	2	AA09		
24	1776.5	79.7	431	8	AD05		
25	1776.5	79.7	431	8	AD05		

26	1770.5	79.4	431	2	AAR97293	Mouse	CRF
27	1770.5	79.4	431	2	Abu62362	Mouse	cor
28	1770.5	79.4	431	5	AAB26583	Mouse	CRF
29	1770.5	79.4	431	5	AAO19431	Murine	co
30	1770.5	79.4	431	6	ABU08079	Mouse	cor
31	1770.5	79.4	431	6	ABG76050	Mouse	cor
32	1770.5	79.4	431	8	ADJ65805	Mouse	cor
33	1770.5	79.4	431	8	ADG029268	Mouse	GPC
34	1770.5	79.4	431	8	ADG050805	mouse	cor
35	1769	79.4	430	5	AAO19432	Murine	co
36	1769	79.4	430	8	ADG050807	mouse	cor
37	1582.5	71.0	428	5	AEO19437	Fish	co
38	1582.5	71.0	428	8	ADG050817	Catfish	C
39	1582	71.0	420	5	AAO19440	Chicken	C
40	1582	71.0	420	8	ADG050823	Chicken	C
41	1578.5	70.8	445	5	AAO19436	Fish	co
42	1578.5	70.8	445	8	ADG050815	Catfish	C
43	1566	70.3	415	2	AAR69519	Human	pit
44	1566	70.3	415	2	AAR97290	Human	CRF
45	1566	70.3	415	2	AAM00159	Human	cor

## ALIGNMENTS

RESULT 1	
AA019435	AA019435 standard; protein; 413 AA.
XX	
AC	AA019435;
XX	DT 10-DEC-2002 (first entry)
XX	
DE	Xenopus corticotrophin releasing factor receptor CRF2R
XX	Human; rat; mouse; sheep; cow; chicken; CRF1R; CRF2R;
KW	corticotrophin releasing factor
KW	muscular atrophy; corticotrophin releasing factor-1
KW	gene therapy.

Xenopus laevis. WO200269908-A2. 12-SEP-2002. 06-MAR-2002; 2002WO-US007416.

06-MAR-2001; 2001US-00799978. (PROC ) PROCTER & GAMBLE CO. Isfort RJ, Sheldon RJ; WPI; 2002-713413/77. N-PSDB; AAL49986.

Identifying candidate compounds for regulating skeletal muscle mass or treating skeletal muscle atrophy by identifying test compounds that bind to, or activate, the corticotropin releasing factor-2 receptor.

Claim 7; Page 142-143; 167pp; English.

The present invention relates to a method of identifying candidate compounds for regulating skeletal muscle mass or function, and comprises contacting a test compound with a corticotropin releasing factor-2 receptor (CRF2R) or with a cell expressing a functional CRF2R, determining whether the test compound binds to, or activates, the CRF2R and identifying the test compounds that bind to, or activates, the CRF2R as candidate compounds for regulating skeletal muscle mass or function. The method is useful for preparing a medicament for treating skeletal muscle atrophy or for prophylactic treatment of muscular dystrophies. The present invention is a corticotropin releasing factor receptor

XX Sequence 413 AA;

Query Match 100.0%; Score 2229; DB 5; Length 413;  
Best Local Similarity 100.0%; Pred. No. 6.9e-217;  
Matches 413; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MDSTIEIIIDDEFDANCSLLDAFQDSFLISESSSEFGFCGPICSATIDQIGTCWPRSLAG 60  
Db 1 MDSTIEIIIDDEFDANCSLLDAFQDSFLISESSSEFGFCGPICSATIDQIGTCWPRSLAG 60

Qy 61 ELVERPCPDSENGIRNTANVRECFCENTWASMYSOCVPILDNKRKYAHYKALI 120  
Db 61 ELVERPCPDSENGIRNTANVRECFCENTWASMYSOCVPILDNKRKYAHYKALI 120

Qy 121 INYLGHCISIALVAFLLPLCRLSTRCLRNIIHWNLTTFILRNIMWLLQMDHNTHE 180  
Db 121 INYLGHCISIALVAFLLPLCRLSTRCLRNIIHWNLTTFILRNIMWLLQMDHNTHE 180

Qy 181 SNEVWCRCITIINYVFTVNTFPMMEVEGGCYLHTAIVMITYSTDKLRKAVFLLFGCICPSPI 240  
Db 181 SNEVWCRCITIINYVFTVNTFPMMEVEGGCYLHTAIVMITYSTDKLRKAVFLLFGCICPSPI 240

Qy 241 IVTWAICLKYENEOCQWIGEKGPKIDYIYQGRVILVLLINFVLNITRILMTKLRAST 300  
Db 241 IVTWAICLKYENEOCQWIGEKGPKIDYIYQGRVILVLLINFVLNITRILMTKLRAST 300

Qy 301 TSETIQYRAKAVATLVLPLIGITYMFLFVNPGEDDVSQIVLYFNSFLQSFQGFVFVVF 360  
Db 301 TSETIQYRAKAVATLVLPLIGITYMFLFVNPGEDDVSQIVLYFNSFLQSFQGFVFVVF 360

Qy 361 YCFLNGEVRSAAARKWHRWDDHSLRVRVARAMSPTSPTRISPHSIKQTAAV 413  
Db 361 YCFLNGEVRSAAARKWHRWDDHSLRVRVARAMSPTSPTRISPHSIKQTAAV 413

XX Sequence 413 AA;

Query Match 100.0%; Score 2229; DB 8; Length 413;  
Best Local Similarity 100.0%; Pred. No. 6.9e-217;  
Matches 413; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MDSTIEIIIDDEFDANCSLLDAFQDSFLISESSSEFGFCGPICSATIDQIGTCWPRSLAG 60  
Db 1 MDSTIEIIIDDEFDANCSLLDAFQDSFLISESSSEFGFCGPICSATIDQIGTCWPRSLAG 60

Qy 61 ELVERPCPDSENGIRNTANVRECFCENTWASMYSOCVPILDNKRKYAHYKALI 120  
Db 61 ELVERPCPDSENGIRNTANVRECFCENTWASMYSOCVPILDNKRKYAHYKALI 120

Qy 121 INYLGHCISIALVAFLLPLCRLSTRCLRNIIHWNLTTFILRNIMWLLQMDHNTHE 180  
Db 121 INYLGHCISIALVAFLLPLCRLSTRCLRNIIHWNLTTFILRNIMWLLQMDHNTHE 180

Qy 181 SNEVWCRCITIINYVFTVNTFPMMEVEGGCYLHTAIVMITYSTDKLRKAVFLLFGCICPSPI 240  
Db 181 SNEVWCRCITIINYVFTVNTFPMMEVEGGCYLHTAIVMITYSTDKLRKAVFLLFGCICPSPI 240

Qy 241 IVTWAICLKYENEOCQWIGEKGPKIDYIYQGRVILVLLINFVLNITRILMTKLRAST 300  
Db 241 IVTWAICLKYENEOCQWIGEKGPKIDYIYQGRVILVLLINFVLNITRILMTKLRAST 300

Qy 301 TSETIQYRAKAVATLVLPLIGITYMFLFVNPGEDDVSQIVLYFNSFLQSFQGFVFVVF 360  
Db 301 TSETIQYRAKAVATLVLPLIGITYMFLFVNPGEDDVSQIVLYFNSFLQSFQGFVFVVF 360

Qy 361 YCFLNGEVRSAAARKWHRWDDHSLRVRVARAMSPTSPTRISPHSIKQTAAV 413  
Db 361 YCFLNGEVRSAAARKWHRWDDHSLRVRVARAMSPTSPTRISPHSIKQTAAV 413

RESULT 2  
ADO50813 standard; protein; 413 AA.  
ADO50813;  
XX US2004101911-A1.  
XX DT 12-AUG-2004 (first entry)  
DE Frog corticotropin releasing factor receptor 2, CRF2R.  
XX Frog; receptor; corticotropin releasing factor receptor; CRF1R; CRF2R;  
KW skeletal muscle; muscle atrophy; skeletal muscle dystrophy;  
KW skeletal muscle hypertrophy; surgery; bed rest; broken bone;  
KW infectious disease; AIDS cachexia.  
XX Xenopus laevis.  
XX US2004101911-A1.  
XX 27-MAY-2004.  
XX 27-AUG-2003; 2003US-00649852.  
XX 06-MAR-2001; 2001US-00799979.  
XX (PROC ) PROCTER & GAMBLE CO.  
XX Isfort RJ, Sheldon RJ;  
WPI: 2004-459890/43.  
DR N-PSDB; ADO50812.  
XX Identifying compounds for regulating skeletal muscle mass or function, by  
PT contacting test compound with vertebrate corticotropin releasing factor 2  
, PT receptors (CRF2R), selecting compounds that bind or activate CRF2R.  
XX  
PS Claim 3; SEQ ID NO 32; 100pp; English.

RESULT 3  
AAQ19438  
ID AAQ19438 Standard; protein; 405 AA.  
XX  
AC AAQ19438;  
XX  
DT 10-DEC-2002 (first entry)



Query Match	81.1%	Score 1807;	DB 8;	Length 405;	CC (CRF2) receptor protein, which can be used to screen for an agonist or antagonist which activates the receptor, or competitively inhibits the binding of the receptor to CRF. The agonist can be used to prevent or treat dementia and obesity, or accelerate stress adaptation. The antagonist can be used to prevent or treat melancholia, anxiety, stress headaches, AIDS, Alzheimer's disease or gastrointestinal disorders
Best Local Similarity	79.9%	Pred. No. 4e-174;			
Matches 330;	Conservative 33;	Mismatches 42;	Indels 8;	Gaps 2;	
Qy	1 MDSTIEFBI1IDEFDANCSLLDAFQDFSLHSBSSSPFGPBCOPYCSATIDQITCPRLSLAG 60				
Db	1 MEVSLIELL--SVEVNCSSLADAFGPAYNSDAL-----EGTCWPRSGAG 52				
	Sequence 411 AA;				
Qy	61 ELVERPCPDSEFNGIYNTENVYRECENGTFASWMNYSCCVPILDNKRYALHYKAI 120	Query Match 80.9%;	Score 1804;	DB 2;	Length 411;
Db	53 RVVARPCPDFFNGVKNSRSAYRCLENTWAFKINTSCEPILERKYPHYKAI 112	Best Local Similarity 80.0%;	Pred. No. 8 3e-174;		
	Matches 333;	Conservative 33;	Mismatches 42;	Indels 8;	Gaps 4;
Qy	121 INYLGHC1SIALVIAFLFLICLRSIRCLRN1HWNLTTFILRNIMWFLQMDHNT 180	1 MDSTIEFBI1IDEFDANCSLLDAFQDFSLHSBSSSPFGPBCOPYCSATIDQITCPRLSLAG 58			
Db	113 INYLGHC1SIALVIAFLFLICLRSIRCLRN1HWNLTTFILRNIMWFLQMDHNT 172	1 MDAALHLHSLL--EANCS--ALAAELLLDGMWOPPLDEGPYSYCNITLUDQIGTCWPRSLA 55			
Qy	181 SNEVACRCITIINYFVVTNFFWMEVEGGYLHTAIVMTYSTDKLRKWFLIGNCIPSP 240	59 AGELVERPCPDSEFNGIYNTENVYRECENGTFASWMNYSCCVPILDNK-RKYALHYK 117			
Db	173 RNEPWCRL1TIVYFVVTNFFWMEVEGGYLHTAIVMTYSTDKLRKWFLIGNCIPCPV 232	56 AGALVERPCPEYNGVKNTNTDRARECLENGTWASKINYSQCEPILDKORKYDLYHRY 115			
Qy	241 IWTWAIKCLLPTENEOQWIGKEPGKVTDYIYQGRVILVLLINFVLNTIRLMTKLRAST 300	118 ALINLYNGLHC1SIALVIAFLFLICLRSIRCLRN1HWNLTTFILRNIMWFLQMDHNT 177			
Db	233 IIAWAVGKL1TNEENQWIGKEPGKVTDYIYQGRVILVLLINFVLNTIRLMTKLRAST 292	116 ALVWNLYLGHCVSVAALVAAPFLFLALRSIRCLRN1HWNLTTFILRNIMWFLQMDHNT 175			
Qy	301 TSETI0YRKAVKATLVLPLIGITYMLFVYNPGEDDSQVLFYFNSPLQSFOGFVFSVF 360	178 IHESENLYWCRCTTINYFVVTNFFWMEVEGGYLHTAIVMTYSTDKLRKWFLIGNCIP 237			
Db	293 TSETI0YRKAVKATLVLPLIGITYMLFVYNPGDDISQIVFVNSPLQSFOGFVFSVF 352	176 VHESENLYWCRCTTINYFVVTNFFWMEVEGGYLHTAIVMTYSTDKLRKWFLIGNCIP 235			
Qy	361 YCFELNGEVRSAAARKWHRWQDHHSILRVYARAMS1PTSPTRISPHSIKQTA 413	238 SPLITVWA1KLFYNEQCWIGKEPGKVDYIYQGRVILVLLINFVLNTIRLMTKLRAST 297			
Db	353 YCFELNGEVRSAAVKWHRWQDHHSILRVYARAMS1PTSPTRISPHSIKQTA 405	236 FPLIVAWA1GKLYYNEQCWIGKEPGKVDYIYQGRVILVLLINFVLNTIRLMTKLRAST 295			
RESULT 5		298 ASTTSETI0YRKAVKATLVLPLIGITYMLFVYNPGEDDSQVLFYFNSPLQSFOGFV 357			
AAW16481	ID AAW16481 standard; protein; 411 AA.	296 ASTTSETI0YRKAVKATLVLPLIGITYMLFVYNPGDDISQIVFVNSPLQSFOGFV 355			
AC AAW16481;		358 SVFYCF1GEVRSARKWHRWQDHHSILRVYARAMS1PTSPTRISPHSIKQTA 413			
DT 20-JUN-1997	(first entry)	Db 356 SVFYCF1GEVRSARKWHRWQDHHSILRVYARAMS1PTSPTRISPHSIKQTA 411			
DE Human corticotrophin releasing factor 2 receptor protein.					
XX Human; corticotrophin; corticotropin; releasing factor 2; CRF2; receptor; screen; agonist; antagonist; activation; inhibition; prevention; treatment; dementia; obesity; acceleration; stress adaptation; melancholia; anxiety; stress; headache; AIDS; acquired immunodeficiency syndrome; Alzheimer's disease; gastrointestinal disorder.					
XX (TAKE ) TAKEDA CHEM IND LTD.					
XX WPI; 1997-230023/21.					
XX N-PSDB; AAT66508.					
XX PCR primer for G protein conjugate type receptor protein DNA - and human corticotrophin releasing factor 2 receptor protein, useful to screen for agonists and antagonists to treat dementia and anxiety.					
XX *PS Claim 8; Page 39-40; 46pp; Japanese.					
XX The present sequence is the human corticotrophin releasing factor 2					
CC					
CC Human; corticotropin releasing factor receptor 2; h15571;					
CC immunomodulatory; vascular; hepatic; antiasthma; antimicrobial; antiinflammatory; immunosuppressive; gene therapy; vaccine; G-protein coupled receptor; GPCR; liver fibrosis; respiratory disorder; infection; chronic inflammatory disease; organ specific autoimmunity; graft rejection; cystic fibrosis.					
CC Homo sapiens.					
CC DR 08-FEB-2001.					
CC N-PSDB; AAT66508.					
XX PT 03-AUG-2000; 2000WO-US021278.					
XX PT 03-AUG-1999; 99US-014616P.					
XX PT 29-FEB-2000; 2000US-00515781.					
XX PA (MILL-) MILLENIUM PHARM INC.					
XX Hodge MR, Lloyd C, Weich NS;					
PI					

XX WPI: 2001-138653/14.  
XX  
XX Nucleic acids encoding a G-prot. coupled receptor polypeptides, useful  
XX for preventing, diagnosing and treating, e.g. liver fibrosis and asthma.  
XX Disclosure; Fig 2: 145pp; English.  
XX  
XX The present sequence is a human G-protein coupled receptor (GPCR) used  
XX for comparison with the seven transmembrane domain of a novel GPCR  
XX designated h15571. h15571 GPCR polynucleotides and polypeptides may be  
XX used in the prevention, treatment and diagnosis of diseases associated  
XX with inappropriate GPCR expression. Such diseases includes immune,  
XX hematological, fibrotic, hepatic and respiratory disorders including  
XX asthma, allergies (e.g. allergic rhinitis and psoriasis), pathogenic  
XX infections, chronic inflammatory diseases, organ-specific autoimmunity,  
XX graft rejection, graft versus host disease, cystic fibrosis and, in  
XX particular, liver fibrosis. The GPCR polypeptides may be used as antigens  
XX in the production of antibodies against GPCR and in assays to identify  
XX modulators (agonists and antagonists) of GPCR expression and activity.  
XX The anti-GPCR antibodies and GPCR antagonists may also be used to down  
XX regulate GPCR expression and activity. The anti-GPCR antibodies may be  
XX used as diagnostic agents for detecting the presence of GPCR polypeptides  
XX in samples

Sequence 411 AA:  
**ISQ** Sequence 411 AA:  
**Query** Match 80.9%; Score 1804; DB 4; Length 411;  
**Best Local Similarity** 80.0%; Pred. No. 8.3e-174;  
**Matches** 333; **Conservative** 33; **Mismatches** 42; **Indels** 8; **Gaps** 4

1	MDSTPFLIDEPDANCSSLLAFOQPSFLHSESSSSFFEGP	YCSATIDQIGTCWRSLL	58
1	MDAALLHSLL--BANCSLL--ALABELLUDGWWGPLDGP	YCSATIDQIGTCWRSAA	55

59	AGBLVVERPCPDSTNGIRINTNTNRYRCPENGNTWSWNTYSOCUPUDNPK-RKYALHVK	117
60	AGBLVVERPCPDSTNGIRINTNTNRYRCPENGNTWSWNTYSOCUPUDNPK-RKYALHVK	117
65	AGBLVVERPCPDSTNGIRINTNTNRYRCPENGNTWSWNTYSOCUPUDNPK-RKYALHVK	115

118 ALIINYLGHCISIALVIAFLFLCLRSIRCLRNIIHWNLTTFIIRNIMFLLOQMDHN 177  
Qy

Db	Qy	Sequenzen
176	VHSNEVWRCR	CTTIFNTYVVTNFWMVVEGCVLTTIAVMTYSTERLKCFLFGMCIP 235
176	VHSNEVWRCR	176 SPLIVTWAICKLPVNEQWIGKEPKYTDIYIGRVLVLLINFTFLNIVRLILTKLR 297

296 ASTTSETIQYRKAVKATLVPLLGLITYMUFFVNPGEDDLSQIMF1YFNNSFLQSFGQFRV 355

356 SVYPCPENGEVRSAVRKRWERWQDHSRLVEMARAMSIPSTRSFHSIKOTAV 411

## RESULT 7 ADC88183

ADC86183 STANARD/ protocol; all PA.  
XX ADC86183;

DT 01-JAN-2004 (First entry)  
 XX Human GPCR protein SEQ ID NO:636.  
 DS human; GPCR; guanosine triphosphate-binding protein coupled receptor;  
 KW gene therapy.  
 KW

*Homo sapiens*.  
S S  
X X  
EP1270724-A2.

Nucleic acids encoding a G-protein coupled receptor polypeptides, useful for preventing, diagnosing and treating, e.g. liver fibrosis and asthma. Disclosure; Fig 2; 145pp; English.

The present sequence is a human G protein-coupled receptor (GPCR) domain. For comparison with the seven transmembrane domain of a novel GPCR designated h15571, h15571 GPCR polypeptides and polypeptides may be used in the prevention and diagnosis of diseases associated with inappropriate GPCR expression. Such diseases includes immune, hematological, fibrotic, and respiratory disorders including, asthma, allergies (e.g. allergic rhinitis and psoriasis), pathogenic infections, chronic inflammatory diseases, organ-specific autoimmunity, graft rejection, graft versus host disease, cystic fibrosis and, in particular, liver fibrosis. The GPCR polypeptides may be used as antigens in the production of antibodies against GPCR and in assays to identify modulators (agonists and antagonists) of GPCR expression and activity. The anti-GPCR antibodies and GPCR antagonists may also be used to down regulate GPCR expression and activity. The anti-GPCR antibodies may be used as diagnostic agents for detecting the presence of GPCR polypeptides in samples.

triphosphate-binding protein coupled receptor (GPCR). A polynucleotide of the invention may have a use in gene therapy. The polynucleotide and polypeptide are useful for preparing a composition for treating a patient in need of increased or suppressed activity or expression of the guanosine triphosphate binding protein coupled receptor. The protein sequences shown in ADC85549-ADC8717 represent GPCR's of the invention.

לונדון, 11 במרץ 1901.

Best Local Similarity 80.0%; Pred. No. 8.3e-174; Mismatches 333; Conservative 33; Nmatches 42; Indels 8; Gaps 4; Matches 333;

59	AGELVERPQDPDSFGVIRYNTTRVYRCPENGWTASWMMYSCQCPILDNK-RECALHYK	117
60	AGALVERPCEPYEVGKONTTNA TRECLINGWTASWMMYSCQEPILDQKQRKYDLYH	115
61	AGALVERPCEPYEVGKONTTNA TRECLINGWTASWMMYSCQEPILDQKQRKYDLYH	115

178 IHSNEVWGRCLITIINYFVVTNFVFFMMFVECCYLHTRAIVMITYSTDCLRKWVFLIGWCIP 237

Db	236	PLIIIVAWAQLKLYENEQCMWFGKEPEPLVDIYQGPIIIVLVLINFLNFVLNFNIVRLMTKL	295
Dv	298	ASTTSETIOYRKAVATVLLPLLGITMYLFFVNPNPGDDVSQIVFYIYNSFLQSQFGFFF	357

296 ASTTSETIGRKAVKATLVILLPLLGITYMLRFVNPGRDDLSQIMFTYIYNFSQGFFFV 355

356 SVYCFNGEVRSAVKRWRQDHSLRVMARAMSIPTSPTRISFSIKQTAAV 411

RESULT 8  
ADO2967  
ID ADO2967 standard; protein; 411 AA.  
XX  
AC  
ADO2967;  
XX



PT Corticotropin-releasing factor-2 receptor, and DNA encoding it - used to  
 PT isolate CRF-2 receptor antagonists for the treatment of cerebrovascular  
 PT disorders, memory disorders and Alzheimer's disease.  
 XX Disclosure; Page 80-82; 109pp; English.

XX Human corticotropin-releasing factor-2 (CRF2) receptor (AAR90576) is a  
 CC membrane-bound G-coupled protein receptor involved in signal  
 CC transduction. It can be produced by expression of encoding cDNA  
 CC (AAT1247) in procarcyotic or eucaryotic host cells. Recombinant CRF2  
 CC receptor is used to screen CRF2 receptor agonists and antagonists of  
 CC therapeutic applin., and to prepare antibodies which specifically bind to  
 CC CRF2 receptors.  
 XX Sequence 411 AA;

Query Match 80.7%; Score 1799; DB 2; Length 411;  
 Best Local Similarity 79.8%; Pred. No. 2.7e-173;  
 Matches 332; Conservative 33; Mismatches 43; Indels 8; Gaps 4;  
 Qy 1 MDSTIFRILIDEFDANGSLLDAFQDSFLHSQSSSSPFFGEGP--YCSATIDQIGTCWPRSL 58  
 Db 1 MDAALIHSLL--EANCSL--ALAEELLDGEGPSSYNTTLDQIGTCWPRSA 55  
 Qy 59 AGELVERPCPDOSFNGTRNTTRVNPREFENGTWASWMWNSQCVPFLDNLK-RKYALHYKI 117  
 Db 56 AGELVERPCPDOSFNGTRNTTRVNPREFENGTWASWMWNSQCVPFLDQKRYDLYHRI 115  
 Qy 118 ALIINTLGHCISILALVAFILFLCIRSICLRLNITHWNLITFLRNWFLQMLDHN 177  
 Db 116 ALIINTLGHCVSAAVAVAFILFLAARSICLRLNITHWNLITFLRNWFLQLVDHE 175  
 Qy 178 IHEISNEWWCRCTTITVNYEVUTNFFNVEGCGYLTAIVMVTYSTDKLKRKVYFLIGWCIP 237  
 Db 176 VHEISNEWWCHCITTTIINYEVUTNFFNVEGCGYLTAIVMVTYSTBLRKCLFLFIGWCIP 235  
 Qy 238 SPLITVTAICKLFYENHQCGWCKEPKGYKIDTYQGRVILVLLNFPLNIVRLMTKL 297  
 Db 236 FPIIVAWAIGKLYYNEQCMWCKEPKGYKIDTYQGRVILVLLNFPLNIVRLMTKL 295  
 Qy 298 ASTTSETIYQYRKAVKATVLLPLGLTMLFVNPGEQDVSQVYIYFNSPLQSFGFVV 357  
 Db 296 ASTTSETIYQYRKAVKATVLLPLGLTMLFVNPGEQDLSQIMFYENSPLSQFGFVV 355  
 Qy 358 SVPYCYLGEVRSAAKTRWHRNODHHSILRVARYRAMSIPSPTRISFHKTQAAV 413  
 Db 356 SVPYCYLGEVRSAAKTRWHRNODHHSILRVPMARAMSIPSPTRISFHKTQAAV 411

## RESULT 10

AA019424 standard; protein; 411 AA.  
 XX AAO19424;

DT 10-DEC-2002 (first entry)

DE Human corticotropin releasing factor receptor CRFRalpha.  
 XX Human; rat; mouse; sheep; cow; chicken; CRF1R; CRF2R;  
 KW skeletal muscle atrophy; corticotropin releasing factor-2 receptor;  
 KW muscular atrophy; corticotropin releasing factor-1 receptor;  
 KW gene therapy.

XX Homo sapiens.

OS WO20029908-A2.

PN 12-SEP-2002.

XX 06-MAR-2002; 2002WO-US007476.

XX 06-MAR-2001; 2001US-00799978.

XX (PROC ) PROCTER & GAMBLE CO.  
 PA  
 XX PA  
 PI Isfort RJ, Sheldon RJ;  
 XX DR WPI: 2002-713413/77.  
 N-PSDB; AAL49875.  
 PT Identifying candidate compounds for regulating skeletal muscle mass or  
 PT treating skeletal muscle atrophy by identifying test compounds that bind  
 PT to, or activate, the corticotropin releasing factor-2 receptor.  
 XX  
 PS Claim 7; Page 95-97; 167pp; English.  
 XX  
 CC The present invention relates to a method of identifying candidate  
 CC compounds for regulating skeletal muscle mass or function, and comprises  
 CC contacting a test compound with a corticotropin releasing factor-2  
 receptor (CRF2R) or with a cell expressing a functional CRF2R,  
 CC determining whether the test compound binds to, or activates, the CRF2R  
 CC and identifying the test compounds that bind to, or activates, the CRF2R  
 CC as candidate compounds for regulating skeletal muscle mass or function.  
 CC The method is useful for preparing a medicament for treating skeletal  
 CC muscle atrophy or for prophylactic treatment of muscular dystrophies. The  
 CC present sequence is a corticotropin releasing factor receptor  
 XX Sequence 411 AA;  
 SQ  
 Query Match 80.7%; Score 1799; DB 5; Length 411;  
 Best Local Similarity 79.8%; Pred. No. 2.7e-173;  
 Matches 332; Conservative 33; Mismatches 43; Indels 8; Gaps 4;  
 Qy 1 MDSTIFEIIIDFADNCSSLDAFQDSFLHSQSSSSPFFGEGP--YCSATIDQIGTCWPRSL 58  
 Db 1 MDAALIHSLL--EANCSL--ALAEELLDGEGPSSYNTTLDQIGTCWPRSA 55  
 Qy 59 AGELVERPCPDOSFNGTRNTTRVNPREFENGTWASWMWNSQCVPFLDNLK-RKYALHYKI 117  
 Db 56 AGELVERPCPDOSFNGTRNTTRVNPREFENGTWASWMWNSQCVPFLDQKRYDLYHRI 115  
 Qy 118 ALIINTLGHCISILALVAFILFLCIRSICLRLNITHWNLITFLRNWFLQMLDHN 177  
 Db 116 ALVNVNLGHCVSAAVAVAFILFLAARSICLRLNITHWNLITFLRNWFLQLVDHE 175  
 Qy 178 IHEISNEWWCRCTTITVNYEVUTNFFNVEGCGYLTAIVMVTYSTDKLKRKVYFLIGWCIP 237  
 Db 176 VHEISNEWWCHCITTTIINYEVUTNFFNVEGCGYLTAIVMVTYSTBLRKCLFLFIGWCIP 235  
 Qy 238 SPLITVTAICKLFYENHQCGWCKEPKGYKIDTYQGRVILVLLNFPLNIVRLMTKL 297  
 Db 236 FPIIVAWAIGKLYYNEQCMWCKEPKGYKIDTYQGRVILVLLNFPLNIVRLMTKL 295  
 Qy 298 ASTTSETIYQYRKAVKATVLLPLGLTMLFVNPGEQDVSQVYIYFNSPLQSFGFVV 357  
 Db 296 ASTTSETIYQYRKAVKATVLLPLGLTMLFVNPGEQDLSQIMFYENSPLSQFGFVV 355  
 Qy 358 SVPYCYLGEVRSAAKTRWHRNODHHSILRVARYRAMSIPSPTRISFHKTQAAV 413  
 Db 356 SVPYCYLGEVRSAAKTRWHRNODHHSILRVPMARAMSIPSPTRISFHKTQAAV 411  
 DE Human corticotropin releasing factor receptor CRFRalpha.  
 KW Human; rat; mouse; sheep; cow; chicken; CRF1R; CRF2R;  
 KW skeletal muscle atrophy; corticotropin releasing factor-2 receptor;  
 KW muscular atrophy; corticotropin releasing factor-1 receptor;  
 KW gene therapy.

XX ABP81806 standard; protein; 411 AA.  
 AC ABP81806;  
 XX DT 04-MAR-2003 (first entry)

XX Human corticotropin releasing factor receptor 2 protein SEQ ID NO: 96.  
 XX ABP81806  
 AC ABP81806;  
 XX DT 04-MAR-2003 (first entry)  
 XX DE Human corticotropin releasing factor receptor 2 protein SEQ ID NO: 96.  
 XX G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;  
 KW G protein-coupled receptor modulator; antibody; immune-related disease;  
 KW growth-related disease; cell regeneration-related disease; AIDS; cancer;

immunological-related cell proliferative disease; autoimmune disease; Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy; osteoporosis; cardiomopathy; inflammation; Crohn's disease; diabetes; graft versus host disease; Parkinson's disease; multiple sclerosis; pain; psoriasis; anxiety; depression; schizophrenia; dementia; memory loss; mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea; hypertension; hypotension; renal disorder; renal disorder; rheumatoid arthritis; trauma; ulcer.

XX Homo sapiens.

XX OS WO200261087-A2.

XX WO200261087-A2.

XX 08-AUG-2002.

XX PD 08-AUG-2002.

XX WO 2001WO-US050107.

XX 19-DEC-2001; 2001WO-US050107.

XX 19-DEC-2000; 2000US-0257144P.

XX (LIFE-) LIFESPAN BIOSCIENCES INC.

XX (LIFE-) LIFESPAN BIOSCIENCES INC.

XX Burner GC, Roush CL, Brown JP;

XX WPI; 2003-046718/04.

XX N-PSDB; ABZ42652.

XX New isolated antigenic peptides e.g., for G protein-coupled receptors (GPCR), useful for diagnosing and designing drugs for treating conditions in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or autoimmune diseases.

XX Disclosure: Fig 1; 5239PP; English.

XX The present invention describes antigenic peptides (I) comprising: (a) any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino acids. Also described: (1) an assay for the detection of a particular G protein-coupled receptor (GPCR) or a candidate polypeptide in a sample; and (2) an isolated antibody having high specificity and high affinity or avidity for a particular GPCR. (I) can be used as GPCR modulators and in gene therapy. The antigenic peptides for GPCRs are useful in detecting an antibody against a particular GPCR, and in the production of specific antibodies. The peptides and antibodies are also useful for detecting the presence or absence of corresponding GPCRs. The antigenic peptides for GPCRs and antibodies are useful for diagnosing and designing drugs for treating immune-related diseases, growth-related diseases, cell regeneration-related disease, immunological-related cell proliferative diseases, or autoimmune diseases e.g. AIDS, Alzheimer's disease, osteoarthritis, bacterial, fungal, protozoal or viral infections, osteoporosis, cancer, cardiomopathy, chronic and acute inflammation, allergies, Crohn's disease, diabetes, graft versus host disease, Parkinson's disease, multiple sclerosis, pain, psoriasis, anxiety, depression, schizophrenia, dementia, mental retardation, memory loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension, hypertension, renal disorders, rheumatoid arthritis, trauma, ulcers, or any other disorder in which GPCRs are involved. The antibodies may be used in immunoassays and immunodiagnostics. ABZ42523 to ABZ42869 encode GPCR Proteins Given in ABP81675 to ABP82018, which are used in the exemplification of the present invention.

Sequence 411 AA;						
SQ	Query	Match	Score	DB	Length	
XXX		80.7%	1799;	6;	411;	
	Best Local Similarity	79.8%	Pred. No.	2.78-173;		
	Matches	332;	Mismatches	43;	Indels	8;
	Conservative	33;			Gaps	4
	Matches	332;				
Qy	1	MDSTIFELIIDFEDANCSLLDAFFQDSFLHSESSSSFFGEGP	-YCSATIDQIGTCWPRSL	58		
	1	MDAIIILHSLI--DANCSL--AFLAELLIDLGWGPGLDPGPYS	NCNTLIDQIGCWPNSA	55		
Qy	59	AGELVERPCPDPSFGNGIRNNTNRYRECNGTNTASWNYNSOC	PTILDK-RKVALHYKI	117		
	56	AGAVERPCPEYFGVKNNTNRYRECNGTNTASWNYNSOC	PTILDK-RKVALHYKI	115		
Ddb						
Qy						
Ddb						

QY	118	ALINNLGHQISILNLVIAFLLFLCLRSIRCLNLTTHWNLITTPILRNIMWFLQIMIDHN	177
Db	116	ALVNVLGHCVSAAVLAFAFLFLAFLSIRCLNTHWNLITTPILRNIMWFLQIMIDHE	175
QY	178	IHESENEWRCRITTYIINYFVVTNFWMFVEGCVLHTAIYMTYSTDKLKRKAVFLFGCIP	237
Db	176	VHESEBVWHCITIIFNYFVVTNFWMFVEGCVLHTAIYMTYSTDKLKRKAVFLFGCIP	235
QY	238	SPIIYTWAICKLKFYNEQCMIGKEPKYKLDIYQGRVILYVLLINFEVLNIVRLMTKL	297
Db	236	FPIIYTWAICKLKFYNEQCMIGKEPKYKLDIYQGRVILYVLLINFEVLNIVRLMTKL	295
QY	298	ASTTBTIOTVKAVATLVLPLIGITMFLFVNGEDDVSSQIVTEYIYNFSFLQSQGFFV	357
Db	296	ASTTSETIOTVKAVATLVLPLIGITMFLFVNGEDDLQSIMTYFNSFLQSQGFFV	355
QY	358	SVFYCFNLGEVRSAARKRKRWHRWDQHSLRVRAVAMSIPTSPTRSFHSIKQTAAV	413
Db	356	SVFYCFNLGEVRSAVRKRKRWHRWDQHSLRVPMARMSIPTSPTRSFHSIKQTAAV	411
RESULT 12			
	ADO-0791		
	ID	ADO-0791 standard; protein; 411 AA.	
	XX		
	AC		
	ADO-0791;		
	XX		
	DT	12-AUG-2004 (first entry)	
	XX		
	DE	Human corticotropin releasing factor receptor 2 alpha.	
	XX		
	KW	Human; receptor; corticotropin releasing factor receptor; CRF1R; CRF2R;	
	KW	skeletal muscle; muscle atrophy; skeletal muscle dystrophy;	
	KW	skeletal muscle hypertrophy; surgery; bed rest; broken bone;	
	KW	infectious disease; AIDS; cachexia.	
	XX		
	OS	Homo sapiens.	
	XX		
	PN	US2004101911-A1.	
	XX		
	PD	27-MAY-2004.	
	XX		
	PF	27-AUG-2003; 2003US-00649852.	
	XX		
	PR	06-MAR-2001; 2001US-00799978.	
	XX		
	PA	(PROC) PROCTER & GAMBLE CO.	
	XX		
	PI	Isefort RJ, Sheldon RJ;	
	XX		
	WPT	2004-45990/43.	
	DR	N-PSDB; ADO50790.	
	XX		
	PT	Identifying compounds for regulating skeletal muscle mass or function, by	
	PT	contracting test compound with vertebrate corticotropin releasing factor2	
	PT	receptors (CRF2R), selecting compounds that bind or activate CRF2R.	
	XX		
PS	Claim 3: SEQ ID NO 10: 1000pp: English.		

The invention relates to identifying candidate compounds for regulating skeletal muscle mass or function, comprising contacting a test compound with vertebrate corticotropin releasing factor 2 receptors (CRF 2 R), determining if the compound binds to or activates CRF2R, selecting compounds that bind or activate CRF 2 R, and determining if compound increases muscle mass or function in muscle atrophy model. Also included are identifying candidate therapeutic compounds from a group of one or more candidate compounds which have been previously determined to bind to or activate a vertebrate CRF 2 R (comprising administering the candidate compound to a non-human animal and determining whether the candidate compound regulates skeletal muscle mass or function in the animal), increasing skeletal muscle mass or function in a subject in which such an increase is desirable (comprising identifying a subject in which an increase in muscle mass or function is desirable and

administering to the subject a safe and effective amount of a CRF 2 R agonist, a purified antibody specific for a CRF2R (where the antibody is a chimaeric or human antibody), and a pharmaceutical composition comprising a safe and effective amount of a CRF2R agonist and carrier. The methods are useful for identifying candidate compounds for regulating skeletal muscle mass or function, for increasing skeletal muscle mass or function (in a subject in which an increase is desirable), for identifying candidate compounds that are potentially useful in the treatment of skeletal muscle dystrophy and for identifying compounds that prolong or augment the agonist-induced activation of CRFR2 or of a CRFR1 signal transduction pathway. The compound is useful for treating skeletal muscle hypertrophy and for modulating skeletal muscle atrophy induced by e.g. surgery, bed rest, broken bones, infectious disease or AIDS cachexia. The present sequence represents a corticotropin releasing factor receptor.

Sequence 411 AA;  
 SQ      Sequence 411 AA;  
 Query Match      80.7%;      Score 1799;      DB 8;      Length 411;  
 Best Local Similarity      79.8%;      Pred. No. 2.7e-173;  
 Matches 332;      Conservative 33;      Mismatches 43;      Indels 8;  
 Gaps 4

56	AGALVERPCBEYFGVKNTTRNAYRECLENGTWASKINYSQCEPILDDKQRKYDLHYRI	115
118	ALINYNLGHCSISALALVIAFLFLCLRSCLRCRNLNITHWNLLITTFILRNIMWFLQMDHN	177
116	ALVNYNLGHCVSVALVAFLFLCLRSCLRCRNLNITHWNLLITTFILRNIMWFLQLVDHE	175
178	IHEBSNEWVRCRITIENYFVVMFVEGCVLHTATVMTYSTDKRKWVFLIGWCIP	237
176	VHEBSNEWVHCITIENYFVVMFVEGCVLHTATVMTYSERLRKCLFLIGWCIP	235
238	SPILTWAIKCLKFYENEOCGWKGPKYIDYIXYGRVILVLLINFEFLNIVRLMLTKLR	297
236	FPIITVAIAGKLYTENEQCMWFGEKPGDLVYDIXYGSPIIILVLLINFEFLNIVRLMLTKLR	295

RESULT 13  
ADQ9168  
ADQ89168 standard; protein; 411 AA.

AC ADQ9168;  
XX 21-OCT-2004 (first entry)  
XX Human urological disorder related protein 2543 SEQ:120.  
XX

urological disorder; uropathic; cytostatic; urinary incontinence; benign prostatic hyperplasia; human.  
*Homo sapiens*.  
 WO2004065576-A2

XX 05-AUG-2004 .  
PD 14-JAN-2004 ; 2004WO-US000750 .  
XX 15-JAN-2003 ; 2003US-0440318P .  
PP

04-FEB-2003 ; 200303US-0444783P  
27-MAR-2003 ; 200303US-04579015P  
08-MAY-2003 ; 200303US-0468775P  
19-MAY-2003 ; 200303US-0471614P  
16-JUN-2003 ; 200303US-0478424P  
16-JUL-2003 ; 200303US-0485529P  
30-JUL-2003 ; 200303US-0491156P  
02-SEP-2003 ; 200303US-0495594P  
26-SEP-2003 ; 200303US-0506332P  
(MILL-) MILLENNIUM PHARM INC.  
Karichelli V, Silos-Santiago  
WPI: 2004-5621767/54.  
11-NOV-2003 ; 200303US-0506332P

Use of polypeptides related to 211 or for identifying a comp disorder or identifying and the disorder.

Claim 1: SEQ ID NO 120; 542ppx

method for identifying a comm  
disorder; (2) a method for id  
disorder; and (3) a method for  
disorder. The compound has un  
peptides related to urolidine  
compound capable of treating  
having a urological disorder  
disorder. Disorders include u  
hyperplasia. The present seq  
related protein, which is use  
invention.

Best Local Similarity 79.8%;  
Matches 332; Conservative

59 AGELVERPCPDNSFNGIRYNT  
60 : : : : : : : : : : : : : : : :  
56 AGALVERPCPEYFNGVKYNT  
118 AVLINVIGHCISILAVIA

238 SP1IVTWAICKLFYENNEOCQY  
 239 FP1IVAWAIGKLYYENNEOCQY  
 298 ASTTSETTIOYRKAVKATLV

296	b	ASTTSETIQRKAVKATLV
358	Y	SFYFCFLNGEVRSAARKRMW
356	b	SFYCFFNGEVRSAVRKRMW

04-FEB-2003 ; 2003US-0444783P.  
27-MAR-2003 ; 2003US-0457901P.  
08-MAY-2003 ; 2003US-0468775P.  
19-MAY-2003 ; 2003US-0471614P.  
15-JUN-2003 ; 2003US-0478742P.  
18-JUL-2003 ; 2003US-0488529P.  
30-JUL-2003 ; 2003US-0491156P.  
02-SEP-2003 ; 2003US-0499594P.  
26-SEP-2003 ; 2003US-0506334P.

(MILL-) MILLENNIUM PHARM INC.  
Karatchebi V, Silos-Santiago I, Eliasof SD,  
WPI: 2004-562167/54.

use of polypeptides related to urological disorders, e.g. 44300, 54181, 211 or for identifying a compound capable of treating a urological disorder or identifying and treating a subject having a urological disorder.

method for identifying a compound capable of treating a urological disorder; (2) a method for identifying a subject having a urological disorder; and (3) a method for treating a subject having a urological disorder; the compound has uropathic and cytostatic activities. The polypeptides related to urological disorders are useful for identifying a compound capable of treating a urological disorder, identifying a subject having a urological disorder, or treating a subject having a urological disorder. Disorders include urinary incontinence and benign prostatic hyperplasia. The present sequence represents a human urological disorder related protein, which is used in the exemplification of the present invention.

Best local Simililarity 79.8%; Pred. No. 2.7e-173;  
Matches 332; Conservative 33; Mismatches 43; Indels 8; Gaps 5

296	ASTSETIQYRKATKATVLLPLIGITYMLEFFVNGEDDLISQIMIYENSFLQSQGFFV	3		
358	SVFYCFNLGEVRSAARKRKRWHRWDHSLRVARAMSITPSPTRISFHSIKQTAAV	413		
356	SVFYCFNLGEVRSAVRKRKRWHRWDHSLRVPMARAMSITPSPTRISFHSIKQTAAV	411		
b				
b				
b				
b				

RESULT 14	XX	SQ Sequence 411 AA;
ABU62363	XX	Query Match 80.4%; Score 1793; DB 2; Length 411;
ID ABU62363 standard; protein; 411 AA.	XX	Best Local Similarity 80.0%; Pred. No. 1.1e-172;
XX	XX	Matches 333; Conservative 30; Mismatches 45; Indels 8; Gaps 4;
AC ABU62363;	XX	1 MDSTTIEIIIDFADNSLLDAFQDSDPLHSESSSSFFGFGGP -YCSATIDQIGTCYPRSL 58
DT 29-AUG-2003 (first entry)	XX	1 MDA---LLSLBANSL--ALAEELLDDGEGPPDPEGPSYCYNTLDDQIGTCYPRSL 55
DE Rat corticotropin release factor receptor, rCRF-R2alpha.	XX	59 AGELVERPCPDSPNGTRYNTTRVYRECENGFTWASMMYNSOCVPILDNK-RKYALHYKI 117
XX	XX	56 PGALVERDPCPEYNGKYNTRNAYRECLENGTWAISRNYSHCEPLDDKQKRYDHYRI 115
Corticotropin release factor; receptor; adrenocorticotrophic hormone;	KW	118 ALINYLGHGICISIALVIAELFLCLISIRCLRNITIHNLLTTEFLRNIMFLQMDHN 177
ACRH; blood flow; blood pressure; vascular bed; coronary blood flow;	KW	116 ALINYLGHGCVSYVALYRAAFLFLVRSIRCLRNITIHNLLTTEFLRNIMFLQMDHN 175
inflammation; vascular permeability; CRF-binding protein; parturition;	KW	178 IHSNSNEWVRCRCLTTIANYFVVTINPFMVEGCVLHTAIWMTYSTDKRKWVPLFINGCIP 237
Alzheimer's disease; chronic fatigue syndrome; appetite; alertness; rat;	KW	176 VHEGNEWVRCRCLTTIANYFVVTINPFMVEGCVLHTAIWMTYSTDKRKWVPLFINGCIP 235
respiratory system; learning performance; depression; anxiety; memory;	KW	238 SPLITVWACKLFLYENEQCCWIGKEPKYIDTYQGRYLVLLINFLNFYFLNTYRILMTKL R 297
hypothalamic pituitary adrenal function; endocrine disorder; swelling;	KW	298 ASTTSSETIQRKAVKATVLLPLGLITMLFTVNPGDDVSQVFLFNSFLQSQFQFFV 357
central nervous system disorder; CRF; rCRF-R2alpha.	XX	296 ASTTSSETIQRKAVKATVLLPLGLITMLFTVNPGDDVSQVFLFNSFLQSQFQFFV 355
Rattus sp.	OS	236 CPIVAVAWGKLTYENEQCCWIGKEPKDADYIYQGPILVLLINFLNFYFLNTYRILMTKL R 295
XX	XX	356 SVFYCFENGEVRSALARKEWHRMOPDHARLVRPVARAMSIPTSPRISPTSPRISPTSIKQTA AV 411
US2003032587-A1.	PN	RESULT 15
13-FEB-2003.	PD	AAO19428 standard; protein; 411 AA.
26-MAR-2001; 2001US-00818009.	XX	AAO19428
13-JUN-1995; 95US-0028444P.	PR	XX
11-AUG-1995; 95US-0002223P.	PR	AC AAO19428;
12-JUN-1996; 96WO-US010240.	PR	XX
10-DEC-1997; 97US-00981189.	XX	10-DEC-2002 (first entry)
(SALK ) SALK INST BIOLOGICAL STUDIES.	PA	XX
Vale WW, Vaughan J, Donaldson CJ, Lewis KA, Sawchenko P;	PI	Rat corticotropin releasing factor receptor CRF2Ralpha.
Rivier JEF, Perrin MH;	PI	XX
WPI; 1997-077344/07.	DR	XX
XX	XX	Human; rat; mouse; sheep; cow; chicken; CRF1R, CRF2R;
Urocortin peptide(s) related to urotensin and corticotropin-releasing	CC	KW skeletal muscle atrophy; corticotropin releasing factor-2 receptor;
factor - for increasing ACTH and beta-endorphin levels, lowering blood	CC	KW muscular dystrophy; corticotropin releasing factor-1 receptor;
pressure and improving mood, memory and learning performance.	CC	gene therapy.
XX	XX	XX
Disclosure, Page 27-28; 34pp; English.	PS	Rattus norvegicus.
XX	XX	OS
The invention relates to a human urocortin (Ucn) peptide or an analogous	CC	XX
peptide having only conservative substitutions to the amino acid	CC	XX
residues in it, or an N-terminally shortened fragment of either which is	CC	PN WO200269308-A2.
biologically active to increase adrenocorticotrophic hormone (ACTH)	CC	XX
production. Human urocortin or its N-terminally shortened antagonist	CC	PD 12-SEP-2002.
peptide are useful for modifying blood flow and/or blood pressure and is	CC	XX
further useful for modulating blood flow in a desired vascular bed. Human	CC	PP 06-MAR-2002; 2002KO-US007476.
urocortin is also useful for increasing coronary blood flow and for	CC	XX
decreasing swelling and/or inflammation and/or vascular permeability. A	CC	PR 06-MAR-2001; 2001US-00799978.
CRF-binding protein blocking compound is useful for increasing the in-	CC	XX
vivo level of CRF and/or Ucn. The amount of CRF-binding protein blocking	CC	PA (PROC ) PROCTER & GAMBLE CO.
compound is sufficient to promote parturition in a pregnant female. The	CC	XX
amount of the compound administered is effective so as to result in an	CC	PI Isfort RJ, Sheldon RJ;
increase in free endogenous CRF and/or Ucn in the brain which causes	CC	XX
improvement in short to medium term memory in a subject afflicted with	CC	DR WPI; 2002-713413/77.
Alzheimer's disease, relief from chronic fatigue syndrome, suppression of	CC	XX
appetite, stimulation of the respiratory system, improvement in learning	CC	XX
performance, improvement in memory, improvement in alertness, reduction	CC	PT Identifying candidate compounds for regulating skeletal muscle mass or
of depression and/or lessening of anxiety. The compound is administered	CC	PT treating skeletal muscle atrophy by identifying test compounds that bind
so that it reaches the brain. Human urocortin is useful for evaluating	CC	PT to, or activate, the corticotropin releasing factor-2 receptor.
hypothalamic pituitary adrenal function in mammals with suspected	CC	XX
endocrine or central nervous system pathology. Human urocortin antibodies	CC	CC sequence represents the amino acid sequence of the rat corticotropin
are useful in diagnostic methods and systems for detecting the level of	CC	CC release factor receptor, rCRF-R2alpha.
Ucn polypeptide, for immunoaffinity or affinity chromatography	CC	CC purification of Ucn, and also in human therapeutic methods. The present
sequence represents the amino acid sequence of the rat corticotropin	CC	CC sequence represents the amino acid sequence of the rat corticotropin

XX The present invention relates to a method of identifying candidate  
 CC compounds for regulating skeletal muscle mass or function, and comprises  
 CC contacting a test compound with a corticotropin releasing factor-2  
 CC receptor (CRF2R) or with a cell expressing a functional CRF2R,  
 CC determining whether the test compound binds to, or activates, the CRF2R  
 CC and identifying the test compounds that bind to, or activates, the CRF2R  
 CC as candidate compounds for regulating skeletal muscle mass or function.  
 CC The method is useful for preparing a medicament for treating skeletal  
 CC muscle atrophy or for prophylactic treatment of muscular dystrophies. The  
 CC present sequence is a corticotropin releasing factor receptor  
 XX sequence.

SQ Sequence 411 AA:

Query Match 80.4%; Score 1793; DB 5; Length 411;  
 Best Local Similarity 80.0%; Pred. No. 1.1e-17;  
 Matches 333; Conservative 30; Mismatches 45; Indels 8; Gaps 4;  
 Qy 1 MDSTIPILLIDBFDANSLLDAFQDSPLHSSESSSFFGEGP-YCSATIDQIGTCMPSL 58  
 Db 1 MDAA--LLSLEANSL--ALAEELLDGEGPPDGGSYSCNTLDDQIGTCMPSA 55  
 Qy 59 AGSLVERPCPDSFNGIYNTTPNRYCFCENGTWASWNTYQCVPILDNK-RKYALHYKI 117  
 Db 56 PGALVERPCPBEYNGIKNTNAYRECLENGTWASRINYSHCEPILDQKRYDHYRI 115  
 Qy 118 ALININYLGHCTISLAVIAFLFLCIRSICRNLTHWNLJTTFLIRNIMMFLQDIDHN 177  
 Db 116 ALININYLGHCVSVVALVAFLFLFLVRSICRNLTHWNLJTTFLIRNIMMFLQDIDHE 175  
 Qy 178 IHESENWCRCTTINYFVTNPFMVEGCFHPTAIVMITYSTDKLRKWVPLFGWCIP 237  
 Db 176 VHEGNEWCRCTTINYFVTNPFMVEGCFHPTAIVMITYSTDKLRKWVPLFGWCIP 235  
 Qy 238 SPLITVWAIKLFYENECWIGKEPGKXIDTYQGRVTLNFTVRLMTKL 297  
 Db 236 CPIAVAVAGLJYENSCWFGKEPGLDNDYQGPILVLLNFVFLNIVRLMTKL 295  
 Qy 298 ASITSETIYRKAVKATLVLPLIGITYMLFFVNPGSDDVSQIVFYFNSPLQSFGFV 357  
 Db 296 ASITSETIYRKAVKATLVLPLIGITYMLFFVNPGEDDSIVFYFNSPLQSFGFV 355  
 Qy 358 SVFVCPFNGEVRSAAKWRHRMDDHSLRVYRAMSIPSTSRTISFSIKQTAAV 413  
 Db 356 SVFVCPFNGEVRSAAKWRHRMDDHSLRVYRAMSIPSTSRTISFSIKQTAAV 411

Search completed: August 20, 2005, 00:25:30  
 Job time : 168 secs

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